SEQUENCE LISTING

<110> GLYCOFI, INC.

<120> METHODS TO ENGINEER MAMMALIAN-TYPE CARBOHYDRATE STRUCTURES

<130> GFI/102 PCT

<140> PCT/US02/41510
<141> 2002-12-24

<150> 60/344,169
<151> 2001-12-27

<160> 106

<170> PatentIn Ver. 2.1

<210> 1
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<400> 1
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<210> 2
<211> 36
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 2
agaatttggt gggtaagaat tccarcacca ytcrtg 36

<210> 3
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 3
cctaagctgg tatgcgttct ctttgccata tc 32

<210> 4
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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gcggcataaa caataataga tgctataaag 30

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<220>
<223> Description of Artificial Sequence: Primer

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aattaaccct cactaaaggg 20

<210> 6
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<220>
<223> Description of Artificial Sequence: Primer

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gtaatacgac tcactatagg gc 22

<210> 7
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<220>
<223> Description of Artificial Sequence: Primer

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ccacatcatc cgtgctacat atag 24

<210> 8
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acgaggcaag ctaaacagat ctcgaagtat cgagggttat ccag 44

<210> 9
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
ccatccagtg tcgaaaacga gccaatggtt catgtctata aatc 44

<210> 10
<211> 24
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<213> Artificial Sequence

<220>
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<400> 10
agcctcagcg ccaacaagcg atgg 24

<210> 11
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
ctggataacc ctcgatactt cgagatctgt ttagcttgcc tcgt 44

<210> 12
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
gatttataga catgaaccat tggctcgttt tcgacactgg atgg 44

<210> 13
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 13
atcctttacc gatgctgtat 20

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
ataacagtat gtgttacacg cgtgtag 27

<210> 15
<211> 36
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
tcctggcgcg ccttcccgag agaactggcc tccctc 36

<210> 16
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
aattaattaa ccctagccct ccgctgtatc caacttg 37

<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
aatgagatga ggctccgcaa tggaactg 28

<210> 18
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
ctgattgctt atcaacgaga attccttg 28

<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
tgttggtttc tcagatgatc agttggtg 28

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
agagagagat ggctttcttt tctccctgg 29

<210> 21
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
aaatcaagtg gatgaaggac atgtggc 27

<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
agcgatgcta taggcagtct ttgcagag 28

<210> 23
<211> 4
<212> PRT
<213> Saccharomyces cerevisiae

<400> 23
His Asp Glu Leu
1

<210> 24
<211> 458
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MOD_RES
<222> (304)..(318)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (416)..(436)
<223> Variable amino acid

<400> 24
Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
1 5 10 15

Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
20 25 30

Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
35 40 45

Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
50 55 60

Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
65 70 75 80

Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
85 90 95

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
100 105 110

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
115 120 125

Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
130 135 140

Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
145 150 155 160

Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
165 170 175

Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
180 185 190

```
Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
        195                 200                 205

Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
    210                 215                 220

Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
225                 230                 235                 240

Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
                245                 250                 255

Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
            260                 265                 270

His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
        275                 280                 285

Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa
    290                 295                 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Val
305                 310                 315                 320

Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
                325                 330                 335

Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
            340                 345                 350

Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
        355                 360                 365

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
    370                 375                 380

Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
385                 390                 395                 400

Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Xaa
                405                 410                 415

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            420                 425                 430

Xaa Xaa Xaa Xaa Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
        435                 440                 445

Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
    450                 455
```

<210> 25
<211> 458
<212> PRT
<213> Saccharomyces cerevisiae

<400> 25

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Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
 1               5                  10                  15

Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
            20                  25                  30

Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
        35                  40                  45

Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
    50                  55                  60

Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
65                  70                  75                  80

Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
                85                  90                  95

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
            100                 105                 110

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
        115                 120                 125

Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
    130                 135                 140

Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
145                 150                 155                 160

Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
                165                 170                 175

Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
            180                 185                 190

Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
        195                 200                 205

Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
    210                 215                 220

Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
225                 230                 235                 240

Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
                245                 250                 255

Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
            260                 265                 270

His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
        275                 280                 285

Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
    290                 295                 300
```

```
Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
305                 310                 315                 320

Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
                325                 330                 335

Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
            340                 345                 350

Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
        355                 360                 365

Ser Leu  His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
    370                 375                 380

Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
385                 390                 395                 400

Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
                405                 410                 415

Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala
            420                 425                 430

Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
        435                 440                 445

Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
    450                 455
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<210> 26
<211> 443
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MOD_RES
<222> (333)..(347)
<223> Variable amino acid

<400> 26

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Trp Gln Asp Leu Lys Asp Gly Val Arg Tyr Val Ile Phe Asp Cys Arg
  1               5                  10                  15

Ala Asn Leu Ile Val Met Pro Leu Leu Ile Leu Phe Glu Ser Met Leu
             20                  25                  30

Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys
         35                  40                  45

Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp
     50                  55                  60

Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly
 65                  70                  75                  80
```

```
His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp
                 85                  90                  95

His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr
            100                 105                 110

Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp
        115                 120                 125

Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val
    130                 135                 140

Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr
145                 150                 155                 160

Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu
                165                 170                 175

Lys Lys His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Phe Met
            180                 185                 190

Cys Cys Ala Ser Tyr Arg Val His Ser Ile Phe Val Leu Arg Leu Phe
        195                 200                 205

Asn Asp Pro Val Ala Met Val Leu Leu Phe Leu Ser Ile Asn Leu Leu
    210                 215                 220

Leu Ala Gln Arg Trp Gly Trp Gly Ser Leu Ala Leu Val Ile Ser Ala
225                 230                 235                 240

Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu Tyr Phe
                245                 250                 255

Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn Val Ile
            260                 265                 270

Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val Ala Val
        275                 280                 285

Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu His Cys Ala
    290                 295                 300

Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn Trp Gln
305                 310                 315                 320

Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa Xaa Xaa Xaa
                325                 330                 335

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Val Thr Arg Tyr
            340                 345                 350

Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His Pro Leu Arg
        355                 360                 365

Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile Pro Phe Val
    370                 375                 380
```

```
Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg Ser Leu His
385                 390                 395                 400

Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile Leu Ile Phe
                405                 410                 415

Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr Val Leu His
            420                 425                 430

Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser
        435                 440
```

<210> 27
<211> 373
<212> PRT
<213> Homo sapiens

<400> 27

```
Trp Gln Glu Arg Arg Leu Leu Leu Arg Glu Pro Arg Tyr Thr Leu Leu
  1               5                  10                  15

Val Ala Ala Cys Leu Cys Leu Ala Glu Val Gly Ile Thr Phe Trp Val
             20                  25                  30

Ile His Arg Val Ala Tyr Thr Glu Ile Asp Trp Lys Ala Tyr Met Ala
         35                  40                  45

Glu Val Glu Gly Val Gly Thr Tyr Asp Tyr Thr Gln Leu Gln Gly Asp
     50                  55                  60

Thr Gly Pro Leu Val Tyr Pro Ala Gly Phe Val Tyr Ile Phe Met Gly
 65                  70                  75                  80

Leu Tyr Tyr Ala Thr Ser Arg Gly Thr Asp Ile Arg Met Ala Gln Asn
                85                  90                  95

Ile Phe Ala Val Leu Tyr Leu Ala Thr Leu Leu Leu Val Phe Leu Ile
            100                 105                 110

Tyr His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Phe Met Cys
        115                 120                 125

Cys Ala Ser Tyr Arg Val His Ser Ile Phe Val Leu Arg Leu Phe Asn
    130                 135                 140

Asp Pro Val Ala Met Val Leu Leu Phe Leu Ser Ile Asn Leu Leu Leu
145                 150                 155                 160

Ala Gln Arg Trp Gly Trp Gly Cys Cys Phe Phe Ser Leu Ala Val Ser
                165                 170                 175

Val Lys Met Asn Val Leu Leu Phe Ala Pro Gly Leu Leu Phe Leu Leu
            180                 185                 190

Leu Thr Gln Phe Gly Phe Arg Gly Ala Leu Pro Lys Leu Gly Ile Cys
        195                 200                 205
```

```
Ala Gly Leu Gln Val Val Leu Gly Leu Pro Phe Leu Leu Glu Asn Pro
    210                 215                 220

Ser Gly Tyr Leu Ser Arg Ser Phe Asp Leu Gly Arg Gln Phe Leu Phe
225                 230                 235                 240

His Trp Thr Val Asn Trp Arg Phe Leu Pro Glu Ala Leu Phe Leu His
                245                 250                 255

Arg Ala Phe His Leu Ala Leu Leu Thr Ala His Leu Thr Leu Leu Leu
            260                 265                 270

Leu Phe Ala Leu Cys Arg Trp His Arg Thr Gly Glu Ser Ile Leu Ser
        275                 280                 285

Leu Leu Arg Asp Pro Ser Lys Arg Lys Val Pro Pro Gln Pro Leu Thr
    290                 295                 300

Pro Asn Gln Ile Val Ser Thr Leu Phe Thr Ser Asn Phe Ile Gly Ile
305                 310                 315                 320

Cys Phe Ser Arg Ser Leu His Tyr Gln Phe Tyr Val Trp Tyr Phe His
                325                 330                 335

Thr Leu Pro Tyr Leu Leu Trp Ala Met Pro Ala Arg Trp Leu Thr His
            340                 345                 350

Leu Leu Arg Leu Leu Val Leu Gly Leu Ile Glu Leu Ser Trp Asn Thr
        355                 360                 365

Tyr Pro Ser Thr Ser
    370
```

<210> 28
<211> 269
<212> PRT
<213> Saccharomyces cerevisiae

<400> 28

```
Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
  1               5                  10                  15

Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
             20                  25                  30

Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
         35                  40                  45

Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
     50                  55                  60

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
 65                  70                  75                  80

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
                 85                  90                  95
```

```
Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
            100                 105                 110

Tyr Tyr Leu Leu His Pro Trp Cys Val Val Leu Ala Cys Leu Ser Lys
        115                 120                 125

Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys Phe Thr
    130                 135                 140

Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala Ser Arg
145                 150                 155                 160

Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val Ile Ser
                165                 170                 175

Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu Tyr
            180                 185                 190

Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn Val
        195                 200                 205

Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val Ala
    210                 215                 220

Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu His Cys
225                 230                 235                 240

Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn Trp
                245                 250                 255

Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe
            260                 265
```

<210> 29
<211> 258
<212> PRT
<213> Drosophila virilis

<400> 29

```
Ile Lys Tyr Leu Ala Phe Glu Pro Ala Ala Leu Pro Ile Val Ser Val
  1               5                  10                  15

Leu Ile Val Leu Ala Glu Ala Val Ile Asn Val Leu Val Ile Gln Arg
             20                  25                  30

Val Pro Tyr Thr Glu Ile Asp Trp Lys Ala Tyr Met Gln Glu Cys Glu
         35                  40                  45

Gly Phe Leu Asn Gly Thr Thr Asn Tyr Ser Leu Leu Arg Gly Asp Thr
     50                  55                  60

Gly Pro Leu Val Tyr Pro Ala Ala Phe Val Tyr Ile Tyr Ser Gly Leu
 65                  70                  75                  80

Tyr Tyr Leu Thr Gly Gln Gly Thr Asn Val Arg Leu Ala Gln Tyr Ile
                 85                  90                  95
```

```
Phe Ala Cys Ile Tyr Leu Leu Gln Met Cys Leu Val Leu Arg Leu Tyr
            100                 105                 110

Thr Lys Ser Arg Lys Val Pro Pro Tyr Val Leu Val Leu Ser Ala Phe
        115                 120                 125

Thr Ser Tyr Arg Ile His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp
    130                 135                 140

Pro Val Ala Ile Leu Leu Leu Tyr Ala Ala Leu Asn Leu Phe Leu Asp
145                 150                 155                 160

Gln Arg Trp Thr Leu Gly Ser Ile Cys Tyr Ser Leu Ala Val Gly Val
                165                 170                 175

Lys Met Asn Ile Leu Leu Phe Ala Pro Ala Leu Leu Leu Phe Tyr Leu
            180                 185                 190

Ala Asn Leu Gly Val Leu Arg Thr Leu Val Gln Leu Thr Ile Cys Ala
        195                 200                 205

Val Leu Gln Leu Phe Ile Gly Ala Pro Phe Leu Arg Thr His Pro Met
    210                 215                 220

Glu Tyr Leu Arg Gly Ser Phe Asp Leu Gly Arg Ile Phe Glu His Lys
225                 230                 235                 240

Trp Thr Val Asn Tyr Arg Phe Leu Ser Lys Glu Leu Phe Glu Gln Arg
                245                 250                 255

Glu Phe
```

<210> 30
<211> 267
<212> PRT
<213> Saccharomyces cerevisiae

<400> 30

```
Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro Leu
  1               5                  10                  15

Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys Val
            20                  25                  30

Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu Met
        35                  40                  45

Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly Thr
    50                  55                  60

Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met Met
65                  70                  75                  80

Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val Phe
                85                  90                  95
```

```
Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys Tyr
            100                 105                 110

Tyr Leu Leu His Trp Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu
        115                 120                 125

His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu
    130                 135                 140

Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala Ser Arg Cys His
145                 150                 155                 160

Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val Ile Ser Ala Thr
                165                 170                 175

Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu Tyr Phe Pro
            180                 185                 190

Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn Val Ile Leu
        195                 200                 205

Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val Ala Val Ala
    210                 215                 220

Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu His Cys Ala Phe
225                 230                 235                 240

Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn Trp Gln Met
                245                 250                 255

Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe
            260                 265
```

<210> 31
<211> 257
<212> PRT
<213> Drosophila melanogaster

<400> 31

```
Lys Tyr Leu Leu Leu Glu Pro Ala Ala Leu Pro Ile Val Gly Leu Phe
  1               5                  10                  15

Val Leu Leu Ala Glu Leu Val Ile Asn Val Val Val Ile Gln Arg Val
             20                  25                  30

Pro Tyr Thr Glu Ile Asp Trp Val Ala Tyr Met Gln Glu Cys Glu Gly
         35                  40                  45

Phe Leu Asn Gly Thr Thr Asn Tyr Ser Leu Leu Arg Gly Asp Thr Gly
     50                  55                  60

Pro Leu Val Tyr Pro Ala Ala Phe Val Tyr Ile Tyr Ser Ala Leu Tyr
 65                  70                  75                  80

Tyr Val Thr Ser His Gly Thr Asn Val Arg Leu Ala Gln Tyr Ile Phe
                 85                  90                  95
```

Ala Gly Ile Tyr Leu Leu Gln Leu Ala Leu Val Leu Arg Leu Tyr Ser
100 105 110

Lys Ser Arg Lys Val Pro Pro Tyr Val Leu Val Leu Ser Ala Phe Thr
115 120 125

Ser Tyr Arg Ile His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Pro
130 135 140

Val Ala Val Leu Leu Leu Tyr Ala Ala Leu Asn Leu Phe Leu Asp Arg
145 150 155 160

Arg Trp Thr Leu Gly Ser Thr Phe Phe Ser Leu Ala Val Gly Val Lys
165 170 175

Met Asn Ile Leu Leu Phe Ala Pro Ala Leu Leu Leu Phe Tyr Leu Ala
180 185 190

Asn Leu Gly Leu Leu Arg Thr Ile Leu Gln Leu Ala Val Cys Gly Val
195 200 205

Ile Gln Leu Leu Leu Gly Ala Pro Phe Leu Leu Thr His Pro Val Glu
210 215 220

Tyr Leu Arg Gly Ser Phe Asp Leu Gly Arg Ile Phe Glu His Lys Trp
225 230 235 240

Thr Val Asn Tyr Arg Phe Leu Ser Arg Asp Val Phe Glu Asn Arg Thr
245 250 255

Phe

<210> 32
<211> 1377
<212> DNA
<213> Saccharomyces cerevisiae

<400> 32
atggaaggtg aacagtctcc gcaaggtgaa aagtctctgc aaaggaagca atttgtcaga 60
cctccgctgg atctgtggca ggatctcaag gacggtgtgc gctacgtgat cttcgattgt 120
agggccaatc ttatcgttat gccccttttg attttgttcg aaagcatgct gtgcaagatt 180
atcattaaga aggtagctta cacagagatc gattacaagg cgtacatgga gcagatcgag 240
atgattcagc tcgatggcat gctggactac tctcaggtga gtggtggaac gggcccgctg 300
gtgtatccag caggccacgt cttgatctac aagatgatgt actggctaac agagggaatg 360
gaccacgttg agcgcgggca agtgtttttc agatacttgt atctccttac actggcgtta 420
caaatggcgt gttactacct tttacatcta ccaccgtggt gtgtggtctt ggcgtgcctc 480
tctaaaagat tgcactctat ttacgtgcta cggttattca atgattgctt cactactttg 540
tttatggtcg tcacggtttt gggggctatc gtggccagca ggtgccatca gcgccccaaa 600
ttaaagaagt cccttgcgct ggtgatctcc gcaacataca gtatggctgt gagcattaag 660
atgaatgcgc tgttgtattt ccctgcaatg atgatttctc tattcatcct taatgacgcg 720
aacgtaatcc ttactttgtt ggatctcgtt gcgatgattg catggcaagt cgcagttgca 780
gtgcccttcc tgcgcagctt tccgcaacag tacctgcatt gcgcttttaa tttcggcagg 840
aagtttatgt accaatggag tatcaattgg caaatgatgg atgaagaggc tttcaatgat 900
aagaggttcc acttggccct tttaatcagc cacctgatag cgctcaccac actgttcgtc 960
acaagatacc ctcgcatcct gcccgattta tggtcttccc tgtgccatcc gctgaggaaa 1020
aatgcagtgc tcaatgccaa tcccgccaag actattccat tcgttctaat cgcatccaac 1080

```
ttcatcggcg tcctattttc aaggtccctc cactaccagt ttctatcctg gtatcactgg 1140
actttgccta tactgatctt ttggtcggga atgcccttct tcgttggtcc catttggtac 1200
gtcttgcacg agtggtgctg gaattcctat ccaccaaact cacaagcaag cacgctattg 1260
ttggcattga atactgttct gttgcttcta ttggccttga cgcagctatc tggttcggtc 1320
gccctcgcca aaagccatct tcgtaccacc agctctatgg aaaaaaagct caactga    1377
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<210> 33
<211> 458
<212> PRT
<213> Saccharomyces cerevisiae

<400> 33

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Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
  1               5                  10                  15

Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
             20                  25                  30

Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
         35                  40                  45

Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
     50                  55                  60

Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
 65                  70                  75                  80

Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
             85                  90                  95

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
            100                 105                 110

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
        115                 120                 125

Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
    130                 135                 140

Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
145                 150                 155                 160

Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
                165                 170                 175

Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
            180                 185                 190

Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
        195                 200                 205

Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
    210                 215                 220

Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
225                 230                 235                 240
```

```
Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
                245                 250                 255

Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
            260                 265                 270

His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
        275                 280                 285

Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
    290                 295                 300

Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
305                 310                 315                 320

Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
                325                 330                 335

Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
            340                 345                 350

Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
        355                 360                 365

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
    370                 375                 380

Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
385                 390                 395                 400

Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
                405                 410                 415

Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala
            420                 425                 430

Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
        435                 440                 445

Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
    450                 455
```

<210> 34
<211> 1395
<212> DNA
<213> Pichia pastoris

<400> 34

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atgcctccga tagagccagc tgaaaggcca aagcttacgc tgaaaaatgt tatcggtgat 60
ctagtggctc ttattcaaaa cgttttattt aacccagatt ttagtgtctt cgttgcacct 120
cttttatggt tagctgattc cattgttatc aaggtgatca ttggcactgt ttcctacaca 180
gatattgatt tttcttcata tatgcaacaa atctttaaaa ttcgacaagg agaattagat 240
tatagcaaca tatttggtga caccggtcca ttggtttacc cagccggcca tgttcatgct 300
tactcagtac tttcgtggta cagtgatggt ggagaagacg tcagtttcgt tcaacaagca 360
tttggttggt tatacctagg ttgcttgtta ctatccatca gctcctactt tttctctggc 420
ttagggaaaa tacctccggt ttatttttgtt ttgttggtag cgtccaagag actgcattca 480
atatttgtat tgagactctt caatgactgt ttaacaacat ttttgatgtt ggcaactata 540
```

```
atcatccttc aacaagcaag tagctggagg aaagatggca caactattcc attatctgtc 600
cctgatgctg cagatacgta cagtttagcc atctctgtaa agatgaatgc gctgctatac 660
ctcccagcat tcctactact catatatctc atttgtgacg aaaatttgat taaagccttg 720
gcacctgttc tagttttgat attggtgcaa gtaggagtcg gttattcgtt cattttaccg 780
ttgcactatg atgatcaggc aaatgaaatt cgttctgcct actttagaca ggcttttgac 840
tttagtcgcc aatttcttta taagtggacg gttaattggc gctttttgag ccaagaaact 900
ttcaacaatg tccattttca ccagctcctg tttgctctcc atattattac gttagtcttg 960
ttcatcctca agttcctctc tcctaaaaac attggaaaac cgcttggtag atttgtgttg 1020
gacattttca aattttggaa gccaacctta tctccaacca atattatcaa cgacccagaa 1080
agaagcccag attttgttta caccgtcatg gctactacca acttaatagg ggtgcttttt 1140
gcaagatctt tacactacca gttcctaagc tggtatgcgt tctctttgcc atatctcctt 1200
tacaaggctc gtctgaactt tatagcatct attattgttt atgccgctca cgagtattgc 1260
tggttggttt tcccagctac agaacaaagt tccgcgttgt tggtatctat cttactactt 1320
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aaaaagaata cataa                                                  1395
```

<210> 35
<211> 464
<212> PRT
<213> Pichia pastoris

<400> 35

```
Met Pro Pro Ile Glu Pro Ala Glu Arg Pro Lys Leu Thr Leu Lys Asn
  1               5                  10                  15

Val Ile Gly Asp Leu Val Ala Leu Ile Gln Asn Val Leu Phe Asn Pro
             20                  25                  30

Asp Phe Ser Val Phe Val Ala Pro Leu Leu Trp Leu Ala Asp Ser Ile
         35                  40                  45

Val Ile Lys Val Ile Ile Gly Thr Val Ser Tyr Thr Asp Ile Asp Phe
     50                  55                  60

Ser Ser Tyr Met Gln Gln Ile Phe Lys Ile Arg Gln Gly Glu Leu Asp
 65                  70                  75                  80

Tyr Ser Asn Ile Phe Gly Asp Thr Gly Pro Leu Val Tyr Pro Ala Gly
                 85                  90                  95

His Val His Ala Tyr Ser Val Leu Ser Trp Tyr Ser Asp Gly Gly Glu
            100                 105                 110

Asp Val Ser Phe Val Gln Gln Ala Phe Gly Trp Leu Tyr Leu Gly Cys
        115                 120                 125

Leu Leu Leu Ser Ile Ser Ser Tyr Phe Phe Ser Gly Leu Gly Lys Ile
    130                 135                 140

Pro Pro Val Tyr Phe Val Leu Leu Val Ala Ser Lys Arg Leu His Ser
145                 150                 155                 160

Ile Phe Val Leu Arg Leu Phe Asn Asp Cys Leu Thr Thr Phe Leu Met
                165                 170                 175

Leu Ala Thr Ile Ile Ile Leu Gln Gln Ala Ser Ser Trp Arg Lys Asp
            180                 185                 190
```

```
Gly Thr Thr Ile Pro Leu Ser Val Pro Asp Ala Ala Asp Thr Tyr Ser
        195                 200                 205

Leu Ala Ile Ser Val Lys Met Asn Ala Leu Leu Tyr Leu Pro Ala Phe
    210                 215                 220

Leu Leu Leu Ile Tyr Leu Ile Cys Asp Glu Asn Leu Ile Lys Ala Leu
225                 230                 235                 240

Ala Pro Val Leu Val Leu Ile Leu Val Gln Val Gly Val Gly Tyr Ser
                245                 250                 255

Phe Ile Leu Pro Leu His Tyr Asp Asp Gln Ala Asn Glu Ile Arg Ser
            260                 265                 270

Ala Tyr Phe Arg Gln Ala Phe Asp Phe Ser Arg Gln Phe Leu Tyr Lys
        275                 280                 285

Trp Thr Val Asn Trp Arg Phe Leu Ser Gln Glu Thr Phe Asn Asn Val
    290                 295                 300

His Phe His Gln Leu Leu Phe Ala Leu His Ile Ile Thr Leu Val Leu
305                 310                 315                 320

Phe Ile Leu Lys Phe Leu Ser Pro Lys Asn Ile Gly Lys Pro Leu Gly
                325                 330                 335

Arg Phe Val Leu Asp Ile Phe Lys Phe Trp Lys Pro Thr Leu Ser Pro
            340                 345                 350

Thr Asn Ile Ile Asn Asp Pro Glu Arg Ser Pro Asp Phe Val Tyr Thr
        355                 360                 365

Val Met Ala Thr Thr Asn Leu Ile Gly Val Leu Phe Ala Arg Ser Leu
    370                 375                 380

His Tyr Gln Phe Leu Ser Trp Tyr Ala Phe Ser Leu Pro Tyr Leu Leu
385                 390                 395                 400

Tyr Lys Ala Arg Leu Asn Phe Ile Ala Ser Ile Ile Val Tyr Ala Ala
                405                 410                 415

His Glu Tyr Cys Trp Leu Val Phe Pro Ala Thr Glu Gln Ser Ser Ala
            420                 425                 430

Leu Leu Val Ser Ile Leu Leu Leu Ile Leu Ile Leu Ile Phe Thr Asn
        435                 440                 445

Glu Gln Leu Phe Pro Ser Gln Ser Val Pro Ala Glu Lys Lys Asn Thr
    450                 455                 460
```

<210> 36
<211> 418
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (209)..(223)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (235)..(246)
<223> Variable amino acid

<400> 36

```
Arg Pro Lys Leu Thr Leu Lys Asn Val Ile Gly Asp Leu Val Ala Leu
  1               5                  10                  15

Ile Gln Asn Val Leu Phe Asn Pro Asp Phe Ser Val Phe Val Ala Pro
             20                  25                  30

Leu Leu Trp Leu Ala Asp Ser Ile Val Ile Lys Val Ile Ile Gly Thr
         35                  40                  45

Val Ser Tyr Thr Asp Ile Asp Phe Ser Ser Tyr Met Gln Gln Ile Phe
     50                  55                  60

Lys Ile Arg Gln Gly Glu Leu Asp Tyr Ser Asn Ile Phe Gly Asp Thr
 65                  70                  75                  80

Gly Pro Leu Val Tyr Pro Ala Gly His Val His Ala Tyr Ser Val Leu
                 85                  90                  95

Ser Trp Tyr Ser Asp Gly Gly Glu Asp Val Ser Phe Val Gln Gln Ala
            100                 105                 110

Phe Gly Trp Leu Tyr Leu Gly Cys Leu Leu Leu Ser Ile Ser Ser Tyr
        115                 120                 125

Phe Phe Ser Gly Leu Gly Lys Ile Pro Pro Val Tyr Phe Val Leu Leu
    130                 135                 140

Val Ala Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg Leu Phe Asn
145                 150                 155                 160

Asp Cys Leu Thr Thr Phe Leu Met Leu Ala Thr Ile Ile Ile Leu Gln
                165                 170                 175

Gln Ala Ser Ser Trp Arg Lys Asp Gly Thr Thr Ile Pro Leu Ser Val
            180                 185                 190

Pro Asp Ala Ala Asp Thr Tyr Ser Leu Ala Ile Ser Val Lys Met Asn
        195                 200                 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
    210                 215                 220

Asp Glu Asn Leu Ile Lys Ala Leu Ala Pro Xaa Xaa Xaa Xaa Xaa Xaa
225                 230                 235                 240

Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ser Phe Ile Leu Pro Leu His Tyr Asp
                245                 250                 255
```

```
Asp Gln Ala Asn Glu Ile Arg Ser Ala Tyr Phe Arg Gln Ala Phe Asp
            260                 265                 270

Phe Ser Arg Gln Phe Leu Tyr Lys Trp Thr Val Asn Trp Arg Phe Leu
        275                 280                 285

Ser Gln Glu Thr Phe Asn Asn Val His Phe His Gln Leu Leu Phe Ala
    290                 295                 300

Leu His Ile Ile Thr Leu Val Leu Phe Ile Leu Lys Phe Leu Ser Pro
305                 310                 315                 320

Lys Asn Ile Gly Lys Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys
                325                 330                 335

Phe Trp Lys Pro Thr Leu Ser Pro Thr Asn Ile Ile Asn Pro Asp Phe
            340                 345                 350

Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile Gly Val Leu Phe Ala
        355                 360                 365

Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr Ala Phe Ser Leu Pro
    370                 375                 380

Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile Ala Ser Ile Ile Val
385                 390                 395                 400

Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe Pro Ala Thr Glu Gln
            405                 410                 415

Ser Ser
```

<210> 37
<211> 398
<212> PRT
<213> Saccharomyces cerevisiae

<400> 37

```
Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly Val Arg Tyr
  1               5                  10                  15

Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro Leu Leu Ile
             20                  25                  30

Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr
         35                  40                  45

Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu Met Ile Gln
     50                  55                  60

Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro
 65                  70                  75                  80

Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met Met Tyr Trp
                 85                  90                  95
```

```
Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val Phe Phe Arg
            100                 105                 110

Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu
        115                 120                 125

Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu Ser Lys Arg
    130                 135                 140

Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr
145                 150                 155                 160

Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala Ser Arg Cys
                165                 170                 175

His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val Ile Ser Ala
            180                 185                 190

Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu Tyr Phe
        195                 200                 205

Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn Val Ile
    210                 215                 220

Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val Ala Val
225                 230                 235                 240

Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu His Cys Ala
                245                 250                 255

Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn Trp Gln
            260                 265                 270

Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His Leu Ala Leu
        275                 280                 285

Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val Thr Arg Tyr
    290                 295                 300

Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His Pro Leu Arg
305                 310                 315                 320

Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile Pro Phe Val
                325                 330                 335

Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg Ser Leu His
            340                 345                 350

Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile Leu Ile Phe
        355                 360                 365

Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr Val Leu His
    370                 375                 380

Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala Ser
385                 390                 395
```

<210> 38
<211> 387
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (183)..(197)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (209)..(220)
<223> Variable amino acid

<400> 38

```
Ser Val Phe Val Ala Pro Leu Leu Trp Leu Ala Asp Ser Ile Val Ile
  1               5                  10                  15

Lys Val Ile Ile Gly Thr Val Ser Tyr Thr Asp Ile Asp Phe Ser Ser
             20                  25                  30

Tyr Met Gln Gln Ile Phe Lys Ile Arg Gln Gly Glu Leu Asp Tyr Ser
         35                  40                  45

Asn Ile Phe Gly Asp Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val
     50                  55                  60

His Ala Tyr Ser Val Leu Ser Trp Tyr Ser Asp Gly Gly Glu Asp Val
 65                  70                  75                  80

Ser Phe Val Gln Gln Ala Phe Gly Trp Leu Tyr Leu Gly Cys Leu Leu
                 85                  90                  95

Leu Ser Ile Ser Ser Tyr Phe Phe Ser Gly Leu Gly Lys Ile Pro Pro
            100                 105                 110

Val Tyr Phe Val Leu Leu Val Ala Ser Lys Arg Leu His Ser Ile Phe
        115                 120                 125

Val Leu Arg Leu Phe Asn Asp Cys Leu Thr Thr Phe Leu Met Leu Ala
    130                 135                 140

Thr Ile Ile Ile Leu Gln Gln Ala Ser Ser Trp Arg Lys Asp Gly Thr
145                 150                 155                 160

Thr Ile Pro Leu Ser Val Pro Asp Ala Ala Asp Thr Tyr Ser Leu Ala
                165                 170                 175

Ile Ser Val Lys Met Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            180                 185                 190

Xaa Xaa Xaa Xaa Xaa Cys Asp Glu Asn Leu Ile Lys Ala Leu Ala Pro
        195                 200                 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ser Phe Ile
    210                 215                 220
```

```
Leu Pro Leu His Tyr Asp Asp Gln Ala Asn Glu Ile Arg Ser Ala Tyr
225                 230                 235                 240

Phe Arg Gln Ala Phe Asp Phe Ser Arg Gln Phe Leu Tyr Lys Trp Thr
                245                 250                 255

Val Asn Trp Arg Phe Leu Ser Gln Glu Thr Phe Asn Asn Val His Phe
            260                 265                 270

His Gln Leu Leu Phe Ala Leu His Ile Ile Thr Leu Val Leu Phe Ile
        275                 280                 285

Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys Phe Trp Lys Pro Thr
    290                 295                 300

Leu Ser Pro Thr Asn Ile Ile Asn Asp Pro Glu Arg Ser Pro Asp Phe
305                 310                 315                 320

Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile Gly Val Leu Phe Ala
                325                 330                 335

Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr Ala Phe Ser Leu Pro
            340                 345                 350

Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile Ala Ser Ile Ile Val
        355                 360                 365

Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe Pro Ala Thr Glu Gln
    370                 375                 380

Ser Ser Ala
385
```

<210> 39
<211> 373
<212> PRT
<213> Neurospora crassa

<400> 39

```
Ser Lys Leu Ile Pro Pro Ala Leu Phe Leu Val Asp Ala Leu Leu Cys
  1               5                  10                  15

Gly Leu Ile Ile Trp Lys Val Pro Tyr Thr Glu Ile Asp Trp Ala Ala
             20                  25                  30

Tyr Met Glu Gln Val Ser Gln Ile Leu Ser Gly Glu Arg Asp Tyr Thr
         35                  40                  45

Lys Val Arg Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Ala His Val
     50                  55                  60

Tyr Ile Tyr Thr Gly Leu Tyr His Leu Thr Asp Glu Gly Arg Asn Ile
 65                  70                  75                  80

Leu Leu Ala Gln Gln Leu Phe Ala Gly Leu Tyr Met Val Thr Leu Ala
                 85                  90                  95
```

```
Val Val Met Gly Cys Tyr Trp Gln Ala Lys Ala Pro Pro Tyr Leu Phe
            100                 105                 110

Pro Leu Leu Thr Leu Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg
        115                 120                 125

Cys Phe Asn Asp Cys Phe Ala Val Leu Phe Leu Trp Leu Ala Ile Phe
    130                 135                 140

Phe Phe Gln Arg Arg Asn Trp Gln Ala Gly Ala Leu Leu Tyr Thr Leu
145                 150                 155                 160

Gly Leu Gly Val Lys Met Thr Leu Leu Leu Ser Leu Pro Ala Val Gly
                165                 170                 175

Ile Val Leu Phe Leu Gly Ser Gly Ser Phe Val Thr Thr Leu Gln Leu
            180                 185                 190

Val Ala Thr Met Gly Leu Val Gln Ile Leu Ile Gly Val Pro Phe Leu
        195                 200                 205

Ala His Tyr Pro Thr Glu Tyr Leu Ser Arg Ala Phe Glu Leu Ser Arg
    210                 215                 220

Gln Phe Phe Phe Lys Trp Thr Val Asn Trp Arg Phe Val Gly Glu Glu
225                 230                 235                 240

Ile Phe Leu Ser Lys Gly Phe Ala Leu Thr Leu Leu Ala Leu His Val
            245                 250                 255

Leu Val Leu Gly Ile Phe Ile Thr Thr Arg Trp Ile Lys Pro Ala Arg
            260                 265                 270

Lys Ser Leu Val Gln Leu Ile Ser Pro Val Leu Leu Ala Gly Lys Pro
        275                 280                 285

Pro Leu Thr Val Pro Glu His Arg Ala Ala Ala Arg Asp Val Thr Pro
    290                 295                 300

Arg Tyr Ile Met Thr Thr Ile Leu Ser Ala Asn Ala Val Gly Leu Leu
305                 310                 315                 320

Phe Ala Arg Ser Leu His Tyr Gln Phe Tyr Ala Tyr Val Ala Trp Ser
                325                 330                 335

Thr Pro Phe Leu Leu Trp Arg Ala Gly Leu His Pro Val Leu Val Tyr
            340                 345                 350

Leu Leu Trp Ala Val His Glu Trp Ala Trp Asn Val Phe Pro Ser Thr
        355                 360                 365

Pro Ala Ser Ser Ala
    370
```

<210> 40
<211> 390

<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (176)..(190)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (202)..(213)
<223> Variable amino acid

<400> 40

```
Leu Trp Leu Ala Asp Ser Ile Val Ile Lys Val Ile Ile Gly Thr Val
  1               5                  10                  15

Ser Tyr Thr Asp Ile Asp Phe Ser Ser Tyr Met Gln Gln Ile Phe Lys
             20                  25                  30

Ile Arg Gln Gly Glu Leu Asp Tyr Ser Asn Ile Phe Gly Asp Thr Gly
         35                  40                  45

Pro Leu Val Tyr Pro Ala Gly His Val His Ala Tyr Ser Val Leu Ser
     50                  55                  60

Trp Tyr Ser Asp Gly Gly Glu Asp Val Ser Phe Val Gln Gln Ala Phe
 65                  70                  75                  80

Gly Trp Leu Tyr Leu Gly Cys Leu Leu Leu Ser Ile Ser Ser Tyr Phe
                 85                  90                  95

Phe Ser Gly Leu Gly Lys Ile Pro Pro Val Tyr Phe Val Leu Leu Val
            100                 105                 110

Ala Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg Leu Phe Asn Asp
        115                 120                 125

Cys Leu Thr Thr Phe Leu Met Leu Ala Thr Ile Ile Ile Leu Gln Gln
    130                 135                 140

Ala Ser Ser Trp Arg Lys Asp Gly Thr Thr Ile Pro Leu Ser Val Pro
145                 150                 155                 160

Asp Ala Ala Asp Thr Tyr Ser Leu Ala Ile Ser Val Lys Met Asn Xaa
                165                 170                 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Asp
            180                 185                 190

Glu Asn Leu Ile Lys Ala Leu Ala Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        195                 200                 205

Xaa Xaa Xaa Xaa Xaa Tyr Ser Phe Ile Leu Pro Leu His Tyr Asp Asp
    210                 215                 220

Gln Ala Asn Glu Ile Arg Ser Ala Tyr Phe Arg Gln Ala Phe Asp Phe
225                 230                 235                 240
```

```
Ser Arg Gln Phe Leu Tyr Lys Trp Thr Val Asn Trp Arg Phe Leu Ser
                245                 250                 255

Gln Glu Thr Phe Asn Asn Val His Phe His Gln Leu Leu Phe Ala Leu
            260                 265                 270

His Ile Ile Thr Leu Val Leu Phe Ile Leu Lys Phe Leu Ser Pro Lys
        275                 280                 285

Asn Ile Gly Lys Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys Phe
    290                 295                 300

Trp Lys Pro Thr Leu Ser Pro Thr Asn Ile Ile Asn Asp Pro Glu Arg
305                 310                 315                 320

Ser Pro Asp Phe Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile Gly
                325                 330                 335

Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr Ala
            340                 345                 350

Phe Ser Leu Pro Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile Ala
        355                 360                 365

Ser Ile Ile Val Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe Pro
    370                 375                 380

Ala Thr Glu Gln Ser Ser
385                 390
```

<210> 41
<211> 355
<212> PRT
<213> Schizosaccharomyces pombe

<400> 41

```
Leu Leu Leu Leu Glu Ile Pro Phe Val Phe Ala Ile Ile Ser Lys Val
  1               5                  10                  15

Pro Tyr Thr Glu Ile Asp Trp Ile Ala Tyr Met Glu Gln Val Asn Ser
             20                  25                  30

Phe Leu Leu Gly Glu Arg Asp Tyr Lys Ser Leu Val Gly Cys Thr Gly
         35                  40                  45

Pro Leu Val Tyr Pro Gly Gly His Val Phe Leu Tyr Thr Leu Leu Tyr
     50                  55                  60

Tyr Leu Thr Asp Gly Gly Thr Asn Ile Val Arg Ala Gln Tyr Ile Phe
 65                  70                  75                  80

Ala Phe Val Tyr Trp Ile Thr Thr Ala Ile Val Gly Tyr Leu Phe Lys
                 85                  90                  95

Ile Val Arg Ala Pro Phe Tyr Ile Tyr Val Leu Leu Ile Leu Ser Lys
            100                 105                 110
```

```
Arg Leu His Ser Ile Phe Ile Leu Arg Leu Phe Asn Asp Gly Phe Asn
        115                 120                 125

Ser Leu Phe Ser Ser Leu Phe Ile Leu Ser Ser Cys Lys Lys Lys Trp
    130                 135                 140

Val Arg Ala Ser Ile Leu Leu Ser Val Ala Cys Ser Val Lys Met Ser
145                 150                 155                 160

Ser Leu Leu Tyr Val Pro Ala Tyr Leu Val Leu Leu Leu Gln Ile Leu
                165                 170                 175

Gly Pro Lys Lys Thr Trp Met His Ile Phe Val Ile Ile Ile Val Gln
            180                 185                 190

Ile Leu Phe Ser Ile Pro Phe Leu Ala Tyr Phe Trp Ser Tyr Trp Thr
        195                 200                 205

Gln Ala Phe Asp Phe Gly Arg Ala Phe Asp Tyr Lys Trp Thr Val Asn
    210                 215                 220

Trp Arg Phe Ile Pro Arg Ser Ile Phe Glu Ser Thr Ser Phe Ser Thr
225                 230                 235                 240

Ser Ile Leu Phe Leu His Val Ala Leu Leu Val Ala Phe Thr Cys Lys
                245                 250                 255

His Trp Asn Lys Leu Ser Arg Ala Thr Pro Phe Ala Met Val Asn Ser
            260                 265                 270

Met Leu Thr Leu Lys Pro Leu Pro Lys Leu Gln Leu Ala Thr Pro Asn
        275                 280                 285

Phe Ile Phe Thr Ala Leu Ala Thr Ser Asn Leu Ile Gly Ile Leu Cys
    290                 295                 300

Ala Arg Ser Leu His Tyr Gln Phe Tyr Ala Trp Phe Ala Trp Tyr Ser
305                 310                 315                 320

Pro Tyr Leu Cys Tyr Gln Ala Ser Phe Pro Ala Pro Ile Val Ile Gly
                325                 330                 335

Leu Trp Met Leu Gln Glu Tyr Ala Trp Asn Val Phe Pro Ser Thr Lys
            340                 345                 350

Leu Ser Ser
        355
```

<210> 42
<211> 390
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES

<222> (176)..(190)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (202)..(213)
<223> Variable amino acid

<400> 42

```
Leu Trp Leu Ala Asp Ser Ile Val Ile Lys Val Ile Ile Gly Thr Val
  1               5                  10                  15

Ser Tyr Thr Asp Ile Asp Phe Ser Ser Tyr Met Gln Gln Ile Phe Lys
             20                  25                  30

Ile Arg Gln Gly Glu Leu Asp Tyr Ser Asn Ile Phe Gly Asp Thr Gly
         35                  40                  45

Pro Leu Val Tyr Pro Ala Gly His Val His Ala Tyr Ser Val Leu Ser
     50                  55                  60

Trp Tyr Ser Asp Gly Gly Glu Asp Val Ser Phe Val Gln Gln Ala Phe
 65                  70                  75                  80

Gly Trp Leu Tyr Leu Gly Cys Leu Leu Leu Ser Ile Ser Ser Tyr Phe
                 85                  90                  95

Phe Ser Gly Leu Gly Lys Ile Pro Pro Val Tyr Phe Val Leu Leu Val
            100                 105                 110

Ala Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg Leu Phe Asn Asp
        115                 120                 125

Cys Leu Thr Thr Phe Leu Met Leu Ala Thr Ile Ile Ile Leu Gln Gln
    130                 135                 140

Ala Ser Ser Trp Arg Lys Asp Gly Thr Thr Ile Pro Leu Ser Val Pro
145                 150                 155                 160

Asp Ala Ala Asp Thr Tyr Ser Leu Ala Ile Ser Val Lys Met Asn Xaa
                165                 170                 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Asp
            180                 185                 190

Glu Asn Leu Ile Lys Ala Leu Ala Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        195                 200                 205

Xaa Xaa Xaa Xaa Xaa Tyr Ser Phe Ile Leu Pro Leu His Tyr Asp Asp
    210                 215                 220

Gln Ala Asn Glu Ile Arg Ser Ala Tyr Phe Arg Gln Ala Phe Asp Phe
225                 230                 235                 240

Ser Arg Gln Phe Leu Tyr Lys Trp Thr Val Asn Trp Arg Phe Leu Ser
                245                 250                 255
```

```
Gln Glu Thr Phe Asn Asn Val His Phe His Gln Leu Leu Phe Ala Leu
            260                 265                 270

His Ile Ile Thr Leu Val Leu Phe Ile Leu Lys Phe Leu Ser Pro Lys
        275                 280                 285

Asn Ile Gly Lys Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys Phe
    290                 295                 300

Trp Lys Pro Thr Leu Ser Pro Thr Asn Ile Ile Asn Asp Pro Glu Arg
305                 310                 315                 320

Ser Pro Asp Phe Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile Gly
                325                 330                 335

Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr Ala
            340                 345                 350

Phe Ser Leu Pro Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile Ala
        355                 360                 365

Ser Ile Ile Val Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe Pro
    370                 375                 380

Ala Thr Glu Gln Ser Ser
385                 390
```

<210> 43
<211> 363
<212> PRT
<213> Arabidopsis thaliana

<400> 43

```
Leu Ile Leu Ala Asp Ala Ile Leu Val Ala Leu Ile Ile Ala Tyr Val
  1               5                  10                  15

Pro Tyr Thr Lys Ile Asp Trp Asp Ala Tyr Met Ser Gln Val Ser Gly
            20                  25                  30

Phe Leu Gly Gly Glu Arg Asp Tyr Gly Asn Leu Lys Gly Asp Thr Gly
        35                  40                  45

Pro Leu Val Tyr Pro Ala Gly Phe Leu Tyr Val Tyr Ser Ala Val Gln
    50                  55                  60

Asn Leu Thr Gly Gly Glu Val Tyr Pro Ala Gln Ile Leu Phe Gly Val
65                  70                  75                  80

Leu Tyr Ile Val Asn Leu Gly Ile Val Leu Ile Ile Tyr Val Lys Thr
                85                  90                  95

Asp Val Val Pro Trp Trp Ala Leu Ser Leu Leu Cys Leu Ser Lys Arg
            100                 105                 110

Ile His Ser Ile Phe Val Leu Arg Leu Phe Asn Asp Cys Phe Ala Met
        115                 120                 125
```

Thr Leu Leu His Ala Ser Met Ala Leu Phe Leu Tyr Arg Lys Trp His
130 135 140

Leu Gly Met Leu Val Phe Ser Gly Ala Val Ser Val Lys Met Asn Val
145 150 155 160

Leu Leu Tyr Ala Pro Thr Leu Leu Leu Leu Leu Leu Lys Ala Met Asn
165 170 175

Ile Ile Gly Val Val Ser Ala Leu Ala Gly Ala Ala Leu Ala Gln Ile
180 185 190

Leu Val Gly Leu Pro Phe Leu Ile Thr Tyr Pro Val Ser Tyr Ile Ala
195 200 205

Asn Ala Phe Asp Leu Gly Arg Val Phe Ile His Phe Trp Ser Val Asn
210 215 220

Phe Lys Phe Val Pro Glu Arg Val Phe Val Ser Lys Glu Phe Ala Val
225 230 235 240

Cys Leu Leu Ile Ala His Leu Phe Leu Leu Val Ala Phe Ala Asn Tyr
245 250 255

Lys Trp Cys Lys His Glu Gly Gly Ile Ile Gly Phe Met Arg Ser Arg
260 265 270

His Phe Phe Leu Thr Leu Pro Ser Ser Leu Ser Phe Ser Asp Val Ser
275 280 285

Ala Ser Arg Ile Ile Thr Lys Glu His Val Val Thr Ala Met Phe Val
290 295 300

Gly Asn Phe Ile Gly Ile Val Phe Ala Arg Ser Leu His Tyr Gln Phe
305 310 315 320

Tyr Ser Trp Tyr Phe Tyr Ser Leu Pro Tyr Leu Leu Trp Arg Thr Pro
325 330 335

Phe Pro Thr Trp Leu Arg Leu Ile Met Phe Leu Gly Ile Glu Leu Cys
340 345 350

Trp Asn Val Tyr Pro Ser Thr Pro Ser Ser Ser
355 360

<210> 44
<211> 428
<212> DNA
<213> Kluyveromyces lactis

<400> 44
tttgtttaca agctgatacc aacgaacatg aatacaccgg caggtttact gaagattggc 60
aaagctaacc ttttacatcc ttttaccgat gctgtattca gtgcgatgag agtaaacgca 120
gaacaaattg catacatttt acttgttacc aattacattg gagtactatt tgctcgatca 180
ttacactacc aattcctatc ttggtaccat tggacgttac cagtactatt gaattgggcc 240
aatgttccgt atccgctatg tgtgctatgg tacctaacac atgagtggtg ctggaacagc 300
tatccgccaa acgctactgc atccacactg ctacacgcgt gtaacacata ctgttattgg 360

ctgtattctt aagaggaccc gcaaactcga aaagtggtga taacgaaaca acacacgaga 420
aagctgag 428

<210> 45
<211> 141
<212> PRT
<213> Kluyveromyces lactis

<400> 45
Phe Val Tyr Lys Leu Ile Pro Thr Asn Met Asn Thr Pro Ala Gly Leu
1 5 10 15

Leu Lys Ile Gly Lys Ala Asn Leu Leu His Pro Phe Thr Asp Ala Val
20 25 30

Phe Ser Ala Met Arg Val Asn Ala Glu Gln Ile Ala Tyr Ile Leu Leu
35 40 45

Val Thr Asn Tyr Ile Gly Val Leu Phe Ala Arg Ser Leu His Tyr Gln
50 55 60

Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Val Leu Leu Asn Trp Ala
65 70 75 80

Asn Val Pro Tyr Pro Leu Cys Val Leu Trp Tyr Leu Thr His Glu Trp
85 90 95

Cys Trp Asn Ser Tyr Pro Pro Asn Ala Thr Ala Ser Thr Leu Leu His
100 105 110

Ala Cys Asn Thr Tyr Cys Tyr Trp Leu Tyr Ser Glu Asp Pro Gln Thr
115 120 125

Arg Lys Val Val Ile Thr Lys Gln His Thr Arg Lys Leu
130 135 140

<210> 46
<211> 118
<212> PRT
<213> Kluyveromyces lactis

<400> 46
Ala Asn Leu Leu His Pro Phe Thr Asp Ala Val Phe Ser Ala Met Arg
1 5 10 15

Val Asn Ala Glu Gln Ile Ala Tyr Ile Leu Leu Val Thr Asn Tyr Ile
20 25 30

Gly Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr
35 40 45

His Trp Thr Leu Pro Val Leu Leu Asn Trp Ala Asn Val Pro Tyr Pro
50 55 60

Leu Cys Val Leu Trp Tyr Leu Thr His Glu Trp Cys Trp Asn Ser Tyr
65 70 75 80

```
Pro Pro Asn Ala Thr Ala Ser Thr Leu Leu His Ala Cys Asn Thr Tyr
                85                  90                  95

Cys Tyr Trp Leu Tyr Ser Glu Asp Pro Gln Thr Arg Lys Val Val Ile
            100                 105                 110

Thr Lys Gln His Thr Arg
        115
```

<210> 47
<211> 117
<212> PRT
<213> Saccharomyces cerevisiae

<400> 47

```
Ser Ser Leu Cys His Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn
  1               5                  10                  15

Pro Ala Lys Thr Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly
            20                  25                  30

Val Leu Phe Ser Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His
        35                  40                  45

Trp Thr Leu Pro Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val
    50                  55                  60

Gly Pro Ile Trp Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro
65                  70                  75                  80

Pro Asn Ser Gln Ala Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu
                85                  90                  95

Leu Leu Leu Leu Ala Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala
            100                 105                 110

Lys Ser His Leu Arg
        115
```

<210> 48
<211> 113
<212> PRT
<213> Kluyveromyces lactis

<400> 48

```
Phe Thr Asp Ala Val Phe Ser Ala Met Arg Val Asn Ala Glu Gln Ile
  1               5                  10                  15

Ala Tyr Ile Leu Leu Val Thr Asn Tyr Ile Gly Val Leu Phe Ala Arg
            20                  25                  30

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Val
        35                  40                  45
```

```
Leu Leu Asn Trp Ala Asn Val Pro Tyr Pro Leu Cys Val Leu Trp Tyr
     50                  55                  60

Leu Thr His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ala Thr Ala
 65                  70                  75                  80

Ser Thr Leu Leu His Ala Cys Asn Thr Tyr Cys Tyr Trp Leu Tyr Ser
                 85                  90                  95

Glu Asp Pro Gln Thr Arg Lys Val Val Ile Thr Lys Gln His Thr Arg
            100                 105                 110

Lys
```

<210> 49
<211> 106
<212> PRT
<213> Arabidopsis thaliana

<400> 49

```
Phe Ser Asp Val Ser Ala Ser Arg Ile Ile Thr Lys Glu His Val Val
  1               5                  10                  15

Thr Ala Met Phe Val Gly Asn Phe Ile Gly Ile Val Phe Ala Arg Ser
            20                  25                  30

Leu His Tyr Gln Phe Tyr Ser Trp Tyr Phe Tyr Ser Leu Pro Tyr Leu
         35                  40                  45

Leu Trp Arg Thr Pro Phe Pro Thr Trp Leu Arg Leu Ile Met Phe Leu
     50                  55                  60

Gly Ile Glu Leu Cys Trp Asn Val Tyr Pro Ser Thr Pro Ser Ser Ser
 65                  70                  75                  80

Gly Leu Leu Leu Cys Leu His Leu Ile Ile Leu Val Gly Leu Trp Leu
                 85                  90                  95

Ala Pro Ser Val Asp Pro Tyr Gln Leu Lys
            100                 105
```

<210> 50
<211> 1668
<212> DNA
<213> Saccharomyces cerevisiae

<400> 50

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atgaattgca aggcggtaac cattagttta ttactgttgt tatttttaac aagagtatat 60
attcagccga cattctcgtt aatttcagat tgcgatgaaa cttttaatta ttgggaacca 120
ttaaatttat tggtacgtgg atttggtaaa caaacctggg aatattcacc cgagtattct 180
attagatcat gggctttctt attacctttt tactgtattc tttatccagt aaacaaattt 240
actgacctag aaagtcattg gaacttttte atcacaagag catgcttagg ctttttttagt 300
tttatcatgg aatttaaact acatcgtgaa attgcaggca gcttggcatt gcaaatcgca 360
aatatttgga ttattttcca attgtttaat ccgggctggt tccatgcatc tgtggaatta 420
ttgccttctg ccgttgccat gttgttgtat gtaggtgcca ccagacactc tctacgctat 480
```

```
ctgtccactg ggtctacttc taactttacg aaaagtttag cgtacaattt cctggctagt 540
atactaggct ggccatttgt tttaatttta agcttgccat tatgtttaca ttacctttc 600
aaccatagaa ttatttctac catcagaacc gcattcgact gctgtttgat attttcattg 660
actgcatttg ctgtgattgt cactgacagt atattttacg ggaagcttgc tcctgtatca 720
tggaacatct tattttacaa tgtcattaat gcaagtgagg aatctggccc aaatattttc 780
ggggttgagc catggtacta ctatccacta aatttgttac tgaatttccc actgcctgtg 840
ctagttttag ctattttggg aattttccat ttgagattat ggccattatg ggcatcatta 900
ttcacatgga ttgccgtttt cactcaacaa cctcacaaag aggaaagatt tctctatcca 960
atttacgggt taataacttt gagtgcaagt atcgcctttt acaaagtgtt gaatctattc 1020
aatagaaagc cgattcttaa aaaaggtata aagttgtcag ttttattaat tgttgcaggc 1080
caggcaatgt cacggatagt ggctttggtg aacaattaca cagctcctat agccgtctac 1140
gagcaatttt cttcactaaa tcaaggtggt gtgaaggcac cggtagtgaa tgtatgtacg 1200
ggacgtgaat ggtatcactt cccaagttct ttcctgctgc cagataatca taggctaaaa 1260
tttgttaaat ctggatttga tggtcttctt ccaggtgatt ttccagagag tggttctatt 1320
ttcaaaaaga ttagaacttt acctaaggga atgaataaca agaatatata tgataccggt 1380
aaagagtggc cgatcactag atgtgattat tttattgaca tcgtcgcccc aataaatttа 1440
acaaaagacg ttttcaaccc tctacatctg atggataact ggaataagct ggcatgtgct 1500
gcattcatcg acggtgaaaa ttctaagatt ttgggtagag cattttacgt accggagcca 1560
atcaaccgaa tcatgcaaat agttttacca aaacaatgga atcaagtgta cggtgttcgt 1620
tacattgatt actgtttgtt tgaaaaacca actgagacta ctaattga              1668
```

<210> 51
<211> 555
<212> PRT
<213> Saccharomyces cerevisiae

<400> 51

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Met Asn Cys Lys Ala Val Thr Ile Ser Leu Leu Leu Leu Leu Phe Leu
  1               5                  10                  15

Thr Arg Val Tyr Ile Gln Pro Thr Phe Ser Leu Ile Ser Asp Cys Asp
             20                  25                  30

Glu Thr Phe Asn Tyr Trp Glu Pro Leu Asn Leu Leu Val Arg Gly Phe
         35                  40                  45

Gly Lys Gln Thr Trp Glu Tyr Ser Pro Glu Tyr Ser Ile Arg Ser Trp
     50                  55                  60

Ala Phe Leu Leu Pro Phe Tyr Cys Ile Leu Tyr Pro Val Asn Lys Phe
 65                  70                  75                  80

Thr Asp Leu Glu Ser His Trp Asn Phe Phe Ile Thr Arg Ala Cys Leu
                 85                  90                  95

Gly Phe Phe Ser Phe Ile Met Glu Phe Lys Leu His Arg Glu Ile Ala
            100                 105                 110

Gly Ser Leu Ala Leu Gln Ile Ala Asn Ile Trp Ile Ile Phe Gln Leu
        115                 120                 125

Phe Asn Pro Gly Trp Phe His Ala Ser Val Glu Leu Leu Pro Ser Ala
    130                 135                 140

Val Ala Met Leu Leu Tyr Val Gly Ala Thr Arg His Ser Leu Arg Tyr
145                 150                 155                 160
```

```
Leu Ser Thr Gly Ser Thr Ser Asn Phe Thr Lys Ser Leu Ala Tyr Asn
                165                 170                 175

Phe Leu Ala Ser Ile Leu Gly Trp Pro Phe Val Leu Ile Leu Ser Leu
            180                 185                 190

Pro Leu Cys Leu His Tyr Leu Phe Asn His Arg Ile Ile Ser Thr Ile
        195                 200                 205

Arg Thr Ala Phe Asp Cys Cys Leu Ile Phe Ser Leu Thr Ala Phe Ala
    210                 215                 220

Val Ile Val Thr Asp Ser Ile Phe Tyr Gly Lys Leu Ala Pro Val Ser
225                 230                 235                 240

Trp Asn Ile Leu Phe Tyr Asn Val Ile Asn Ala Ser Glu Glu Ser Gly
                245                 250                 255

Pro Asn Ile Phe Gly Val Glu Pro Trp Tyr Tyr Tyr Pro Leu Asn Leu
            260                 265                 270

Leu Leu Asn Phe Pro Leu Pro Val Leu Val Leu Ala Ile Leu Gly Ile
        275                 280                 285

Phe His Leu Arg Leu Trp Pro Leu Trp Ala Ser Leu Phe Thr Trp Ile
    290                 295                 300

Ala Val Phe Thr Gln Gln Pro His Lys Glu Glu Arg Phe Leu Tyr Pro
305                 310                 315                 320

Ile Tyr Gly Leu Ile Thr Leu Ser Ala Ser Ile Ala Phe Tyr Lys Val
                325                 330                 335

Leu Asn Leu Phe Asn Arg Lys Pro Ile Leu Lys Lys Gly Ile Lys Leu
            340                 345                 350

Ser Val Leu Leu Ile Val Ala Gly Gln Ala Met Ser Arg Ile Val Ala
        355                 360                 365

Leu Val Asn Asn Tyr Thr Ala Pro Ile Ala Val Tyr Glu Gln Phe Ser
    370                 375                 380

Ser Leu Asn Gln Gly Gly Val Lys Ala Pro Val Val Asn Val Cys Thr
385                 390                 395                 400

Gly Arg Glu Trp Tyr His Phe Pro Ser Ser Phe Leu Leu Pro Asp Asn
                405                 410                 415

His Arg Leu Lys Phe Val Lys Ser Gly Phe Asp Gly Leu Leu Pro Gly
            420                 425                 430

Asp Phe Pro Glu Ser Gly Ser Ile Phe Lys Lys Ile Arg Thr Leu Pro
        435                 440                 445

Lys Gly Met Asn Asn Lys Asn Ile Tyr Asp Thr Gly Lys Glu Trp Pro
    450                 455                 460
```

```
Ile Thr Arg Cys Asp Tyr Phe Ile Asp Ile Val Ala Pro Ile Asn Leu
465                 470                 475                 480

Thr Lys Asp Val Phe Asn Pro Leu His Leu Met Asp Asn Trp Asn Lys
                485                 490                 495

Leu Ala Cys Ala Ala Phe Ile Asp Gly Glu Asn Ser Lys Ile Leu Gly
            500                 505                 510

Arg Ala Phe Tyr Val Pro Glu Pro Ile Asn Arg Ile Met Gln Ile Val
        515                 520                 525

Leu Pro Lys Gln Trp Asn Gln Val Tyr Gly Val Arg Tyr Ile Asp Tyr
    530                 535                 540

Cys Leu Phe Glu Lys Pro Thr Glu Thr Thr Asn
545                 550                 555


<210> 52
<211> 600
<212> DNA
<213> Pichia pastoris

<400> 52
tggccttcct gtctgctcga tacttccttt tacagtaacc aacatacatg ttctccaaca 60
tgctcttgta tgtattggcc tattctatct tgagacttga tatcaacctt ctatggtatt 120
atttcagact gtgatgaagt gttcaactac tgggagccac tcaacttcat gcttagaggg 180
tttggaaaac agacttggga gtattctcca gagtatgcca tccgatcttg gtcctatcta 240
gtgccacttt ggatagcagg ctatccacca ttgttcctgg atatcccttc ttactacttt 300
ttctactttt tcagactact gctggttatt ttttcattgg ttgcagaagt caagttgtac 360
catagtttga agaaaaatgt cagcagtaag atcagtttct ggtaccttct atttacaacc 420
gttgctccag gaatgtctca tagcacgata gccttattac catcctcttt tgctatggtt 480
tgtcacactt ttgccattag atacgtcatt gattacctac aattaccaac attaatgcgc 540
acaatcagag agactgctgc catctcacca gctcacaaac aacaactagc caactctctc 600


<210> 53
<211> 199
<212> PRT
<213> Pichia pastoris

<400> 53
Trp Pro Ser Cys Leu Leu Asp Thr Ser Phe Tyr Ser Asn Gln His Thr
  1               5                  10                  15

Cys Ser Pro Thr Cys Ser Cys Met Tyr Trp Pro Ile Leu Ser Asp Leu
            20                  25                  30

Ile Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe Asn
        35                  40                  45

Tyr Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln Thr
    50                  55                  60

Trp Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu Val
65                  70                  75                  80
```

```
Pro Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro Ser
                85                  90                  95

Tyr Tyr Phe Phe Tyr Phe Phe Arg Leu Leu Leu Val Ile Phe Ser Leu
            100                 105                 110

Val Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser Ser
        115                 120                 125

Lys Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly Met
    130                 135                 140

Ser His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met Val Cys
145                 150                 155                 160

His Thr Phe Ala Ile Arg Tyr Val Ile Asp Tyr Leu Gln Leu Pro Thr
                165                 170                 175

Leu Met Arg Thr Ile Arg Glu Thr Ala Ala Ile Ser Pro Ala His Lys
            180                 185                 190

Gln Gln Leu Ala Asn Ser Leu
        195
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<210> 54
<211> 140
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (65)..(71)
<223> Variable amino acid

<400> 54

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Ile Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe Asn
  1               5                  10                  15

Tyr Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln Thr
            20                  25                  30

Trp Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu Val
        35                  40                  45

Pro Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro Ser
    50                  55                  60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Leu Leu Val Ile Phe Ser Leu
65                  70                  75                  80

Val Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser Ser
                85                  90                  95

Lys Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly Met
            100                 105                 110
```

Ser His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met Val Cys
115 120 125

His Thr Phe Ala Ile Arg Tyr Val Ile Asp Tyr Leu
130 135 140

<210> 55
<211> 141
<212> PRT
<213> Saccharomyces cerevisiae

<400> 55
Ile Gln Pro Thr Phe Ser Leu Ile Ser Asp Cys Asp Glu Thr Phe Asn
1 5 10 15

Tyr Trp Glu Pro Leu Asn Leu Leu Val Arg Gly Phe Gly Lys Gln Thr
20 25 30

Trp Glu Tyr Ser Pro Glu Tyr Ser Ile Arg Ser Trp Ala Phe Leu Leu
35 40 45

Pro Phe Tyr Cys Ile Leu Tyr Pro Val Asn Lys Phe Thr Asp Leu Glu
50 55 60

Ser His Trp Asn Phe Phe Ile Thr Arg Ala Cys Leu Gly Phe Phe Ser
65 70 75 80

Phe Ile Met Glu Phe Lys Leu His Arg Glu Ile Ala Gly Ser Leu Ala
85 90 95

Leu Gln Ile Ala Asn Ile Trp Ile Ile Phe Gln Leu Phe Asn Pro Gly
100 105 110

Trp Phe His Ala Ser Val Glu Leu Leu Pro Ser Ala Val Ala Met Leu
115 120 125

Leu Tyr Val Gly Ala Thr Arg His Ser Leu Arg Tyr Leu
130 135 140

<210> 56
<211> 127
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (66)..(72)
<223> Variable amino acid

<400> 56
Leu Ile Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe
1 5 10 15

Asn Tyr Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln
20 25 30

```
Thr Trp Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu
        35                  40                  45

Val Pro Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro
    50                  55                  60

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Leu Leu Val Ile Phe Ser
65                  70                  75                  80

Leu Val Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser
                85                  90                  95

Ser Lys Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly
            100                 105                 110

Met Ser His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met
        115                 120                 125
```

<210> 57
<211> 127
<212> PRT
<213> Anopheles gambiae

<400> 57

```
Leu Gln Ser Ala Leu Tyr Ser Ile Ile Ser Asp Cys Asp Glu Thr Tyr
 1               5                  10                  15

Asn Tyr Trp Glu Pro Leu His Tyr Leu Leu Lys Gly Lys Gly Phe Gln
            20                  25                  30

Thr Trp Glu Tyr Ser Pro Glu Phe Ala Leu Arg Ser Tyr Ser Tyr Leu
        35                  40                  45

Trp Leu His Gly Leu Pro Ala Lys Val Leu Gln Leu Met Thr Asp Asn
    50                  55                  60

Gly Val Leu Ile Phe Tyr Phe Val Arg Cys Leu Leu Ala Val Thr Cys
65                  70                  75                  80

Ala Leu Leu Glu Tyr Arg Leu Tyr Arg Ile Leu Gly Arg Lys Cys Gly
                85                  90                  95

Gly Gly Val Ala Ser Leu Trp Leu Leu Phe Gln Leu Thr Ser Ala Gly
            100                 105                 110

Met Phe Ile Ser Ser Ala Ala Leu Leu Pro Ser Ser Phe Ser Met
        115                 120                 125
```

<210> 58
<211> 157
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES

<222> (66)..(72)
<223> Variable amino acid

<400> 58
Leu Ile Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe
1 5 10 15

Asn Tyr Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln
20 25 30

Thr Trp Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu
35 40 45

Val Pro Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro
50 55 60

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Leu Leu Val Ile Phe Ser
65 70 75 80

Leu Val Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser
85 90 95

Ser Lys Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly
100 105 110

Met Ser His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met Val
115 120 125

Cys His Thr Phe Ala Ile Arg Tyr Val Ile Asp Tyr Leu Gln Leu Pro
130 135 140

Thr Leu Met Arg Thr Ile Arg Glu Thr Ala Ala Ile Ser
145 150 155

<210> 59
<211> 154
<212> PRT
<213> Schizosaccharomyces pombe

<400> 59
Leu Thr Ser Ala Ser Phe Arg Val Ile Asp Asp Cys Asp Glu Val Tyr
1 5 10 15

Asn Tyr Trp Glu Pro Leu His Tyr Leu Leu Tyr Gly Tyr Gly Leu Gln
20 25 30

Thr Trp Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Phe Tyr Ile
35 40 45

Ala Leu His Ala Val Pro Gly Phe Leu Ala Arg Gly Leu Gly Leu Ser
50 55 60

Arg Leu His Val Phe Tyr Phe Ile Arg Gly Val Leu Ala Cys Phe Ser
65 70 75 80

Ala Phe Cys Glu Thr Asn Leu Ile Leu Ala Val Ala Arg Asn Phe Asn
85 90 95

```
Arg Ala Val Ala Leu His Leu Thr Ser Val Leu Phe Val Asn Ser Gly
            100                 105                 110

Met Trp Ser Ala Ser Thr Ser Phe Leu Pro Ser Ser Phe Ala Met Asn
        115                 120                 125

Met Val Thr Leu Ala Leu Ser Ala Gln Leu Ser Pro Pro Ser Thr Lys
    130                 135                 140

Arg Thr Val Lys Val Val Ser Phe Ile Thr
145                 150
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<210> 60
<211> 141
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (80)..(86)
<223> Variable amino acid

<400> 60

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Ser Pro Thr Cys Ser Cys Met Tyr Trp Pro Ile Leu Ser Asp Leu Ile
  1               5                  10                  15

Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe Asn Tyr
            20                  25                  30

Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln Thr Trp
        35                  40                  45

Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu Val Pro
    50                  55                  60

Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro Ser Xaa
65                  70                  75                  80

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Leu Leu Val Ile Phe Ser Leu Val
                85                  90                  95

Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser Ser Lys
            100                 105                 110

Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly Met Ser
        115                 120                 125

His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met
    130                 135                 140
```

<210> 61
<211> 143
<212> PRT
<213> Mus musculus

<400> 61
Ala Pro Glu Gly Ser Thr Ala Phe Lys Cys Leu Leu Ser Ala Arg Leu
1 5 10 15

Cys Ala Ala Leu Leu Ser Asn Ile Ser Asp Cys Asp Glu Thr Phe Asn
20 25 30

Tyr Trp Glu Pro Thr His Tyr Leu Ile Tyr Gly Lys Gly Phe Gln Thr
35 40 45

Trp Glu Tyr Ser Pro Val Tyr Ala Ile Arg Ser Tyr Ala Tyr Leu Leu
50 55 60

Leu His Ala Trp Pro Ala Ala Phe His Ala Arg Ile Leu Gln Thr Asn
65 70 75 80

Lys Ile Leu Val Phe Tyr Phe Leu Arg Cys Leu Leu Ala Phe Val Ser
85 90 95

Cys Val Cys Glu Leu Tyr Phe Tyr Lys Ala Val Cys Lys Lys Phe Gly
100 105 110

Leu His Val Ser Arg Met Met Leu Ala Phe Leu Val Leu Ser Thr Gly
115 120 125

Met Phe Cys Ser Ser Ser Ala Phe Leu Pro Ser Ser Phe Cys Met
130 135 140

<210> 62
<211> 141
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (80)..(86)
<223> Variable amino acid

<400> 62
Ser Pro Thr Cys Ser Cys Met Tyr Trp Pro Ile Leu Ser Asp Leu Ile
1 5 10 15

Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe Asn Tyr
20 25 30

Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln Thr Trp
35 40 45

Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu Val Pro
50 55 60

Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro Ser Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Leu Leu Val Ile Phe Ser Leu Val
85 90 95

```
Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser Ser Lys
            100                 105                 110

Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly Met Ser
        115                 120                 125

His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met
    130                 135                 140
```

<210> 63
<211> 143
<212> PRT
<213> Homo sapiens

<400> 63

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Ala Pro Glu Gly Ser Thr Ala Phe Lys Cys Leu Leu Ser Ala Arg Leu
  1               5                  10                  15

Cys Ala Ala Leu Leu Ser Asn Ile Ser Asp Cys Asp Glu Thr Phe Asn
             20                  25                  30

Tyr Trp Glu Pro Thr His Tyr Leu Ile Tyr Gly Glu Gly Phe Gln Thr
         35                  40                  45

Trp Glu Tyr Ser Pro Ala Tyr Ala Ile Arg Ser Tyr Ala Tyr Leu Leu
     50                  55                  60

Leu His Ala Trp Pro Ala Ala Phe His Ala Arg Ile Leu Gln Thr Asn
 65                  70                  75                  80

Lys Ile Leu Val Phe Tyr Phe Leu Arg Cys Leu Leu Ala Phe Val Ser
                 85                  90                  95

Cys Ile Cys Glu Leu Tyr Phe Tyr Lys Ala Val Cys Lys Lys Phe Gly
            100                 105                 110

Leu His Val Ser Arg Met Met Leu Ala Phe Leu Val Leu Ser Thr Gly
        115                 120                 125

Met Phe Cys Ser Ser Ser Ala Phe Leu Pro Ser Ser Phe Cys Met
    130                 135                 140
```

<210> 64
<211> 1656
<212> DNA
<213> Saccharomyces cerevisiae

<400> 64

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atgcgttggt ctgtccttga tacagtgcta ttgaccgtga tttcctttca tctaatccaa 60
gctccattca ccaaggtgga agagagtttt aatattcaag ccattcatga tattttaacc 120
tacagcgtat ttgatatctc ccaatatgac cacttgaaat ttcctggagt agtccctaga 180
acattcgttg gtgctgtgat tattgcaatg ctttcgagac cttatcttta cttgagttct 240
ttgatccaaa cttccaggcc tacgtctata gatgttcaat tggtcgttag ggggattgtt 300
ggcctcacca atgggctttc ttttatctat ttaaagaatt gtttgcaaga tatgtttgat 360
gaaatcactg aaaagaaaaa ggaagaaaat gaagacaagg atatatacat ttacgatagc 420
gctggtacat ggtttctttt atttttaatt ggcagtttcc acctcatgtt ctacagcact 480
```

```
aggactctgc ctaattttgt catgactctg cctctaacca acgtcgcatt ggggtgggtt 540
ttattgggtc gttataatgc agctatattc ctatctgcgc tcgtggcaat tgtatttaga 600
ctggaagtgt cagctctcag tgctggtatt gctctattta gcgtcatctt caagaagatt 660
tctttattcg atgctatcaa attcggtatc tttggcttgg gacttggttc cgccatcagt 720
atcaccgttg attcatattt ctggcaagaa tggtgtctac ctgaggtaga tggtttcttg 780
ttcaacgtgg ttgcgggtta cgcttccaag tggggtgtgg agccagttac tgcttatttc 840
acgcattact tgagaatgat gtttatgcca ccaactgttt tactattgaa ttacttcggc 900
tataaattag cacctgcaaa attaaaaatt gtctcactag catctctttt ccacattatc 960
gtcttatcct ttcaacctca caaagaatgg agattcatca tctacgctgt tccatctatc 1020
atgttgctag gtgccacagg agcagcacat ctatgggaga atatgaaagt aaaaaagatt 1080
accaatgttt tatgtttggc tatattgccc ttatctataa tgacctcctt tttcatttca 1140
atggcgttct tgtatatatc aagaatgaat tatccaggcg gcgaggcttt aacttctttt 1200
aatgacatga ttgtggaaaa aaatattaca aacgctacag ttcatatcag catacctcct 1260
tgcatgacag gtgtcacttt atttggtgaa ttgaactacg gtgtgtacgg catcaattac 1320
gataagactg aaaatacgac tttactgcag gaaatgtggc cctcctttga tttcttgatc 1380
acccacgagc caaccgcctc tcaattgcca ttcgagaata agactaccaa ccattgggag 1440
ctagttaaca caacaaagat gtttactgga tttgacccaa cctacattaa gaactttgtt 1500
ttccaagaga gagtgaatgt tttgtctcta ctcaaacaga tcattttcga caagacccct 1560
accgtttttt tgaaagaatt gacggccaat tcgattgtta aaagcgatgt cttcttcacc 1620
tataagagaa tcaaacaaga tgaaaaaact gattga                          1656
```

<210> 65
<211> 551
<212> PRT
<213> Saccharomyces cerevisiae

<400> 65

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Met Arg Trp Ser Val Leu Asp Thr Val Leu Leu Thr Val Ile Ser Phe
  1               5                  10                  15

His Leu Ile Gln Ala Pro Phe Thr Lys Val Glu Glu Ser Phe Asn Ile
             20                  25                  30

Gln Ala Ile His Asp Ile Leu Thr Tyr Ser Val Phe Asp Ile Ser Gln
         35                  40                  45

Tyr Asp His Leu Lys Phe Pro Gly Val Val Pro Arg Thr Phe Val Gly
     50                  55                  60

Ala Val Ile Ile Ala Met Leu Ser Arg Pro Tyr Leu Tyr Leu Ser Ser
 65                  70                  75                  80

Leu Ile Gln Thr Ser Arg Pro Thr Ser Ile Asp Val Gln Leu Val Val
                 85                  90                  95

Arg Gly Ile Val Gly Leu Thr Asn Gly Leu Ser Phe Ile Tyr Leu Lys
            100                 105                 110

Asn Cys Leu Gln Asp Met Phe Asp Glu Ile Thr Glu Lys Lys Lys Glu
        115                 120                 125

Glu Asn Glu Asp Lys Asp Ile Tyr Ile Tyr Asp Ser Ala Gly Thr Trp
    130                 135                 140

Phe Leu Leu Phe Leu Ile Gly Ser Phe His Leu Met Phe Tyr Ser Thr
145                 150                 155                 160
```

```
Arg Thr Leu Pro Asn Phe Val Met Thr Leu Pro Leu Thr Asn Val Ala
                165                 170                 175

Leu Gly Trp Val Leu Leu Gly Arg Tyr Asn Ala Ala Ile Phe Leu Ser
            180                 185                 190

Ala Leu Val Ala Ile Val Phe Arg Leu Glu Val Ser Ala Leu Ser Ala
        195                 200                 205

Gly Ile Ala Leu Phe Ser Val Ile Phe Lys Lys Ile Ser Leu Phe Asp
    210                 215                 220

Ala Ile Lys Phe Gly Ile Phe Gly Leu Gly Leu Gly Ser Ala Ile Ser
225                 230                 235                 240

Ile Thr Val Asp Ser Tyr Phe Trp Gln Glu Trp Cys Leu Pro Glu Val
                245                 250                 255

Asp Gly Phe Leu Phe Asn Val Val Ala Gly Tyr Ala Ser Lys Trp Gly
            260                 265                 270

Val Glu Pro Val Thr Ala Tyr Phe Thr His Tyr Leu Arg Met Met Phe
        275                 280                 285

Met Pro Pro Thr Val Leu Leu Leu Asn Tyr Phe Gly Tyr Lys Leu Ala
    290                 295                 300

Pro Ala Lys Leu Lys Ile Val Ser Leu Ala Ser Leu Phe His Ile Ile
305                 310                 315                 320

Val Leu Ser Phe Gln Pro His Lys Glu Trp Arg Phe Ile Ile Tyr Ala
                325                 330                 335

Val Pro Ser Ile Met Leu Leu Gly Ala Thr Gly Ala Ala His Leu Trp
            340                 345                 350

Glu Asn Met Lys Val Lys Lys Ile Thr Asn Val Leu Cys Leu Ala Ile
        355                 360                 365

Leu Pro Leu Ser Ile Met Thr Ser Phe Phe Ile Ser Met Ala Phe Leu
    370                 375                 380

Tyr Ile Ser Arg Met Asn Tyr Pro Gly Gly Glu Ala Leu Thr Ser Phe
385                 390                 395                 400

Asn Asp Met Ile Val Glu Lys Asn Ile Thr Asn Ala Thr Val His Ile
                405                 410                 415

Ser Ile Pro Pro Cys Met Thr Gly Val Thr Leu Phe Gly Glu Leu Asn
            420                 425                 430

Tyr Gly Val Tyr Gly Ile Asn Tyr Asp Lys Thr Glu Asn Thr Thr Leu
        435                 440                 445

Leu Gln Glu Met Trp Pro Ser Phe Asp Phe Leu Ile Thr His Glu Pro
    450                 455                 460
```

```
Thr Ala Ser Gln Leu Pro Phe Glu Asn Lys Thr Thr Asn His Trp Glu
465                 470                 475                 480

Leu Val Asn Thr Thr Lys Met Phe Thr Gly Phe Asp Pro Thr Tyr Ile
                485                 490                 495

Lys Asn Phe Val Phe Gln Glu Arg Val Asn Val Leu Ser Leu Leu Lys
            500                 505                 510

Gln Ile Ile Phe Asp Lys Thr Pro Thr Val Phe Leu Lys Glu Leu Thr
        515                 520                 525

Ala Asn Ser Ile Val Lys Ser Asp Val Phe Phe Thr Tyr Lys Arg Ile
    530                 535                 540

Lys Gln Asp Glu Lys Thr Asp
545                 550
```

<210> 66
<211> 840
<212> DNA
<213> Pichia pastoris

<400> 66
tcggtcgaga atgataactg aagaactcaa aatctctcac actttcatcg ttactgtact 60
ggcaatcatt gcatttcagc ctcataaaga atggagattt atagtttaca ttgttccacc 120
acttgtcatc accatatcta cagtacttgc acaactaccc aggagattca caatcgtcaa 180
agttgctgtt tttctcctaa gtttcggctc tttgctcata tccctgtcgt ttcttttcat 240
ctcatcgtat aactacccta ggggtgaagc tttacagcat ttgaacgaga aactccttct 300
actggaccaa agttccctac ctgttgatat taaggttcat atggatgtcc ctgcatgcat 360
gactggggtg actttatttg gttacttgga taactcaaaa ttgaacaatt taagaattgt 420
ctatgataaa acagaagacg agtcgctgga cacaatctgg gattctttca attatgtcat 480
ctccgaaatt gacttggatt cttcgactgc tcccaaatgg gaggggggatt ggctgaagat 540
tgatgttgtc caaggctaca acggcatcaa taaacaatct atcaaaaata caattttcaa 600
ttatggaata cttaaacgga tgataagaga cgcaaccaaa cttgatgttg gatttattcg 660
tacggtcttt cgatccttca taaaatttga tgataaatta ttcatttatg agaggagcag 720
tcaaacctga aaatatatac ctcatttgtt caatttggtg taaagagtgt ggcggataga 780
cttcttgtaa atcaggaaag ctacaattcc aattgctgca aaaaatacca atgcccataa 840

<210> 67
<211> 239
<212> PRT
<213> Pichia pastoris

<400> 67
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Arg Met Ile Thr Glu Glu Leu Lys Ile Ser His Thr Phe Ile Val Thr
  1               5                  10                  15

Val Leu Ala Ile Ile Ala Phe Gln Pro His Lys Glu Trp Arg Phe Ile
            20                  25                  30

Val Tyr Ile Val Pro Pro Leu Val Ile Thr Ile Ser Thr Val Leu Ala
        35                  40                  45

Gln Leu Pro Arg Arg Phe Thr Ile Val Lys Val Ala Val Phe Leu Leu
    50                  55                  60
```

```
Ser Phe Gly Ser Leu Leu Ile Ser Leu Ser Phe Leu Phe Ile Ser Ser
 65                  70                  75                  80

Tyr Asn Tyr Pro Gly Gly Glu Ala Leu Gln His Leu Asn Glu Lys Leu
                85                  90                  95

Leu Leu Leu Asp Gln Ser Ser Leu Pro Val Asp Ile Lys Val His Met
            100                 105                 110

Asp Val Pro Ala Cys Met Thr Gly Val Thr Leu Phe Gly Tyr Leu Asp
        115                 120                 125

Asn Ser Lys Leu Asn Asn Leu Arg Ile Val Tyr Asp Lys Thr Glu Asp
    130                 135                 140

Glu Ser Leu Asp Thr Ile Trp Asp Ser Phe Asn Tyr Val Ile Ser Glu
145                 150                 155                 160

Ile Asp Leu Asp Ser Ser Thr Ala Pro Lys Trp Glu Gly Asp Trp Leu
                165                 170                 175

Lys Ile Asp Val Val Gln Gly Tyr Asn Gly Ile Asn Lys Gln Ser Ile
            180                 185                 190

Lys Asn Thr Ile Phe Asn Tyr Gly Ile Leu Lys Arg Met Ile Arg Asp
        195                 200                 205

Ala Thr Lys Leu Asp Val Gly Phe Ile Arg Thr Val Phe Arg Ser Phe
    210                 215                 220

Ile Lys Phe Asp Asp Lys Leu Phe Ile Tyr Glu Arg Ser Ser Gln
225                 230                 235


<210> 68
<211> 239
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (62)..(80)
<223> Variable amino acid

<400> 68
Arg Met Ile Thr Glu Glu Leu Lys Ile Ser His Thr Phe Ile Val Thr
  1               5                  10                  15

Val Leu Ala Ile Ile Ala Phe Gln Pro His Lys Glu Trp Arg Phe Ile
            20                  25                  30

Val Tyr Ile Val Pro Pro Leu Val Ile Thr Ile Ser Thr Val Leu Ala
        35                  40                  45

Gln Leu Pro Arg Arg Phe Thr Ile Val Lys Val Ala Val Xaa Xaa Xaa
     50                  55                  60
```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Tyr Asn Tyr Pro Gly Gly Glu Ala Leu Gln His Leu Asn Glu Lys Leu
85 90 95

Leu Leu Leu Asp Gln Ser Ser Leu Pro Val Asp Ile Lys Val His Met
100 105 110

Asp Val Pro Ala Cys Met Thr Gly Val Thr Leu Phe Gly Tyr Leu Asp
115 120 125

Asn Ser Lys Leu Asn Asn Leu Arg Ile Val Tyr Asp Lys Thr Glu Asp
130 135 140

Glu Ser Leu Asp Thr Ile Trp Asp Ser Phe Asn Tyr Val Ile Ser Glu
145 150 155 160

Ile Asp Leu Asp Ser Ser Thr Ala Pro Lys Trp Glu Gly Asp Trp Leu
165 170 175

Lys Ile Asp Val Val Gln Gly Tyr Asn Gly Ile Asn Lys Gln Ser Ile
180 185 190

Lys Asn Thr Ile Phe Asn Tyr Gly Ile Leu Lys Arg Met Ile Arg Asp
195 200 205

Ala Thr Lys Leu Asp Val Gly Phe Ile Arg Thr Val Phe Arg Ser Phe
210 215 220

Ile Lys Phe Asp Asp Lys Leu Phe Ile Tyr Glu Arg Ser Ser Gln
225 230 235

<210> 69
<211> 245
<212> PRT
<213> Saccharomyces cerevisiae

<400> 69
Lys Leu Ala Pro Ala Lys Leu Lys Ile Val Ser Leu Ala Ser Leu Phe
1 5 10 15

His Ile Ile Val Leu Ser Phe Gln Pro His Lys Glu Trp Arg Phe Ile
20 25 30

Ile Tyr Ala Val Pro Ser Ile Met Leu Leu Gly Ala Thr Gly Ala Ala
35 40 45

His Leu Trp Glu Asn Met Lys Val Lys Lys Ile Thr Asn Val Leu Cys
50 55 60

Leu Ala Ile Leu Pro Leu Ser Ile Met Thr Ser Phe Phe Ile Ser Met
65 70 75 80

Ala Phe Leu Tyr Ile Ser Arg Met Asn Tyr Pro Gly Gly Glu Ala Leu
85 90 95

```
Thr Ser Phe Asn Asp Met Ile Val Glu Lys Asn Ile Thr Asn Ala Thr
            100                 105                 110

Val His Ile Ser Ile Pro Pro Cys Met Thr Gly Val Thr Leu Phe Gly
        115                 120                 125

Glu Leu Asn Tyr Gly Val Tyr Gly Ile Asn Tyr Asp Lys Thr Glu Asn
    130                 135                 140

Thr Thr Leu Leu Gln Glu Met Trp Pro Ser Phe Asp Phe Leu Ile Thr
145                 150                 155                 160

His Glu Pro Thr Ala Ser Gln Leu Pro Phe Glu Asn Lys Thr Thr Asn
                165                 170                 175

His Trp Glu Leu Val Asn Thr Thr Lys Met Phe Thr Gly Phe Asp Pro
            180                 185                 190

Thr Tyr Ile Lys Asn Phe Val Phe Gln Glu Arg Val Asn Val Leu Ser
        195                 200                 205

Leu Leu Lys Gln Ile Ile Phe Asp Lys Thr Pro Thr Val Phe Leu Lys
    210                 215                 220

Glu Leu Thr Ala Asn Ser Ile Val Lys Ser Asp Val Phe Phe Thr Tyr
225                 230                 235                 240

Lys Arg Ile Lys Gln
                245
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<210> 70
<211> 141
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (43)..(61)
<223> Variable amino acid

<400> 70

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Ile Ile Ala Phe Gln Pro His Lys Glu Trp Arg Phe Ile Val Tyr Ile
  1               5                  10                  15

Val Pro Pro Leu Val Ile Thr Ile Ser Thr Val Leu Ala Gln Leu Pro
             20                  25                  30

Arg Arg Phe Thr Ile Val Lys Val Ala Val Xaa Xaa Xaa Xaa Xaa Xaa
         35                  40                  45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Asn Tyr
     50                  55                  60

Pro Gly Gly Glu Ala Leu Gln His Leu Asn Glu Lys Leu Leu Leu Leu
 65                  70                  75                  80
```

```
Asp Gln Ser Ser Leu Pro Val Asp Ile Lys Val His Met Asp Val Pro
                 85                  90                  95

Ala Cys Met Thr Gly Val Thr Leu Phe Gly Tyr Leu Asp Asn Ser Lys
            100                 105                 110

Leu Asn Asn Leu Arg Ile Val Tyr Asp Lys Thr Glu Asp Glu Ser Leu
        115                 120                 125

Asp Thr Ile Trp Asp Ser Phe Asn Tyr Val Ile Ser Glu
    130                 135                 140
```

<210> 71
<211> 137
<212> PRT
<213> Schizosaccharomyces pombe

<400> 71

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Val Tyr Ser Phe Leu Gly His Lys Glu Trp Arg Phe Ile Ile Tyr Ser
  1               5                  10                  15

Ile Pro Trp Phe Asn Ala Ala Ser Ala Ile Gly Ala Ser Leu Cys Phe
            20                  25                  30

Asn Ala Ser Lys Phe Gly Lys Lys Ile Phe Glu Ile Leu Arg Leu Met
        35                  40                  45

Phe Phe Ser Gly Ile Ile Phe Gly Phe Ile Gly Ser Ser Phe Leu Leu
    50                  55                  60

Tyr Val Phe Gln Tyr Ala Tyr Pro Gly Gly Leu Ala Leu Thr Arg Leu
65                  70                  75                  80

Tyr Glu Ile Glu Asn His Pro Gln Val Ser Val His Met Asp Val Tyr
                85                  90                  95

Pro Cys Met Thr Gly Ile Thr Arg Phe Ser Gln Leu Pro Ser Trp Tyr
            100                 105                 110

Tyr Asp Lys Thr Glu Asp Pro Lys Met Leu Ser Asn Ser Leu Phe Ile
        115                 120                 125

Ser Gln Phe Asp Tyr Leu Ile Thr Glu
    130                 135
```

<210> 72
<211> 143
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (45)..(63)
<223> Variable amino acid

<400> 72

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Leu Ala Ile Ile Ala Phe Gln Pro His Lys Glu Trp Arg Phe Ile Val
 1               5                  10                  15

Tyr Ile Val Pro Pro Leu Val Ile Thr Ile Ser Thr Val Leu Ala Gln
            20                  25                  30

Leu Pro Arg Arg Phe Thr Ile Val Lys Val Ala Val Xaa Xaa Xaa Xaa
        35                  40                  45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
    50                  55                  60

Asn Tyr Pro Gly Gly Glu Ala Leu Gln His Leu Asn Glu Lys Leu Leu
65                  70                  75                  80

Leu Leu Asp Gln Ser Ser Leu Pro Val Asp Ile Lys Val His Met Asp
                85                  90                  95

Val Pro Ala Cys Met Thr Gly Val Thr Leu Phe Gly Tyr Leu Asp Asn
            100                 105                 110

Ser Lys Leu Asn Asn Leu Arg Ile Val Tyr Asp Lys Thr Glu Asp Glu
        115                 120                 125

Ser Leu Asp Thr Ile Trp Asp Ser Phe Asn Tyr Val Ile Ser Glu
    130                 135                 140


<210> 73
<211> 137
<212> PRT
<213> Homo sapiens

<400> 73
Met Ala Leu Tyr Ser Leu Leu Pro His Lys Glu Leu Arg Phe Ile Ile
 1               5                  10                  15

Tyr Ala Phe Pro Met Leu Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr
            20                  25                  30

Leu Leu Asn Asn Tyr Lys Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu
        35                  40                  45

Leu Val Ile Gly His Leu Val Val Asn Ala Ala Tyr Ser Ala Thr Ala
    50                  55                  60

Leu Tyr Val Ser His Phe Asn Tyr Pro Gly Gly Val Ala Met Gln Arg
65                  70                  75                  80

Leu His Gln Leu Val Pro Pro Gln Thr Asp Val Leu Leu His Ile Asp
                85                  90                  95

Val Ala Ala Ala Gln Thr Gly Val Ser Arg Phe Leu Gln Val Asn Ser
            100                 105                 110

Ala Trp Arg Tyr Asp Lys Arg Glu Asp Val Gln Pro Gly Thr Gly Met
        115                 120                 125
```

Leu Ala Tyr Thr His Ile Leu Met Glu
130 135

<210> 74
<211> 1635
<212> DNA
<213> Saccharomyces cerevisiae

<400> 74
atggccattg gcaaaaggtt actggtgaac aaaccagcag aagaatcatt ttatgcttct 60
ccaatgtatg attttttgta tccgtttagg ccagtgggga accaatggct gccagaatat 120
attatctttg tatgtgctgt aatactgagg tgcacaattg gacttggtcc atattctggg 180
aaaggcagtc caccgctgta cggcgatttt gaggctcaga gacattggat ggaaattacg 240
caacatttac cgctttctaa gtggtactgg tatgatttgc aatactgggg attggactat 300
ccaccattaa cagcatttca ttcgtacctt ctgggcctaa ttggatcttt tttcaatcca 360
tcttggtttg cactagaaaa gtcacgtggc tttgaatccc ccgataatgg cctgaaaaca 420
tatatgcgtt ctactgtcat cattagcgac atattgtttt actttcctgc agtaatatac 480
tttactaagt ggcttggtag atatcgaaac cagtcgccca taggacaatc tattgcggca 540
tcagcgattt tgttccaacc ttcattaatg ctcattgacc atgggcactt tcaatataat 600
tcagtcatgc ttggccttac tgcttatgcc ataaataact tattagatga gtattatgct 660
atggcggccg tttgttttgt cctatccatt tgttttaaac aaatggcatt gtattatgca 720
ccgatttttt ttgcttatct attaagtcga tcattgctgt tccccaaatt taacatagct 780
agattgacgg ttattgcgtt tgcaacactc gcaacttttg ctataatatt tgcgccatta 840
tatttcttgg gaggaggatt aaagaatatt caccaatgta ttcacaggat attccctttt 900
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<210> 75
<211> 544
<212> PRT
<213> Saccharomyces cerevisiae

<400> 75
Met Ala Ile Gly Lys Arg Leu Leu Val Asn Lys Pro Ala Glu Glu Ser
1 5 10 15

Phe Tyr Ala Ser Pro Met Tyr Asp Phe Leu Tyr Pro Phe Arg Pro Val
20 25 30

Gly Asn Gln Trp Leu Pro Glu Tyr Ile Ile Phe Val Cys Ala Val Ile
35 40 45

Leu Arg Cys Thr Ile Gly Leu Gly Pro Tyr Ser Gly Lys Gly Ser Pro
50 55 60

```
Pro Leu Tyr Gly Asp Phe Glu Ala Gln Arg His Trp Met Glu Ile Thr
 65                  70                  75                  80

Gln His Leu Pro Leu Ser Lys Trp Tyr Trp Tyr Asp Leu Gln Tyr Trp
                85                  90                  95

Gly Leu Asp Tyr Pro Pro Leu Thr Ala Phe His Ser Tyr Leu Leu Gly
            100                 105                 110

Leu Ile Gly Ser Phe Phe Asn Pro Ser Trp Phe Ala Leu Glu Lys Ser
        115                 120                 125

Arg Gly Phe Glu Ser Pro Asp Asn Gly Leu Lys Thr Tyr Met Arg Ser
    130                 135                 140

Thr Val Ile Ile Ser Asp Ile Leu Phe Tyr Phe Pro Ala Val Ile Tyr
145                 150                 155                 160

Phe Thr Lys Trp Leu Gly Arg Tyr Arg Asn Gln Ser Pro Ile Gly Gln
                165                 170                 175

Ser Ile Ala Ala Ser Ala Ile Leu Phe Gln Pro Ser Leu Met Leu Ile
            180                 185                 190

Asp His Gly His Phe Gln Tyr Asn Ser Val Met Leu Gly Leu Thr Ala
        195                 200                 205

Tyr Ala Ile Asn Asn Leu Leu Asp Glu Tyr Tyr Ala Met Ala Ala Val
    210                 215                 220

Cys Phe Val Leu Ser Ile Cys Phe Lys Gln Met Ala Leu Tyr Tyr Ala
225                 230                 235                 240

Pro Ile Phe Phe Ala Tyr Leu Leu Ser Arg Ser Leu Leu Phe Pro Lys
                245                 250                 255

Phe Asn Ile Ala Arg Leu Thr Val Ile Ala Phe Ala Thr Leu Ala Thr
            260                 265                 270

Phe Ala Ile Ile Phe Ala Pro Leu Tyr Phe Leu Gly Gly Gly Leu Lys
        275                 280                 285

Asn Ile His Gln Cys Ile His Arg Ile Phe Pro Phe Ala Arg Gly Ile
    290                 295                 300

Phe Glu Asp Lys Val Ala Asn Phe Trp Cys Val Thr Asn Val Phe Val
305                 310                 315                 320

Lys Tyr Lys Glu Arg Phe Thr Ile Gln Gln Leu Gln Leu Tyr Ser Leu
                325                 330                 335

Ile Ala Thr Val Ile Gly Phe Leu Pro Ala Met Ile Met Thr Leu Leu
            340                 345                 350

His Pro Lys Lys His Leu Leu Pro Tyr Val Leu Ile Ala Cys Ser Met
        355                 360                 365
```

```
Ser Phe Phe Leu Phe Ser Phe Gln Val His Glu Lys Thr Ile Leu Ile
    370                 375                 380

Pro Leu Leu Pro Ile Thr Leu Leu Tyr Ser Ser Thr Asp Trp Asn Val
385                 390                 395                 400

Leu Ser Leu Val Ser Trp Ile Asn Asn Val Ala Leu Phe Thr Leu Trp
                405                 410                 415

Pro Leu Leu Lys Lys Asp Gly Leu His Leu Gln Tyr Ala Val Ser Phe
            420                 425                 430

Leu Leu Ser Asn Trp Leu Ile Gly Asn Phe Ser Phe Ile Thr Pro Arg
        435                 440                 445

Phe Leu Pro Lys Ser Leu Thr Pro Gly Pro Ser Ile Ser Ser Ile Asn
    450                 455                 460

Ser Asp Tyr Arg Arg Arg Ser Leu Leu Pro Tyr Asn Val Val Trp Lys
465                 470                 475                 480

Ser Phe Ile Ile Gly Thr Tyr Ile Ala Met Gly Phe Tyr His Phe Leu
                485                 490                 495

Asp Gln Phe Val Ala Pro Pro Ser Lys Tyr Pro Asp Leu Trp Val Leu
            500                 505                 510

Leu Asn Cys Ala Val Gly Phe Ile Cys Phe Ser Ile Phe Trp Leu Trp
        515                 520                 525

Ser Tyr Tyr Lys Ile Phe Thr Ser Gly Ser Lys Ser Met Lys Asp Leu
    530                 535                 540
```

<210> 76
<211> 1644
<212> DNA
<213> Pichia pastoris

<400> 76

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tcctattccg gcttcaacac ccctccaatg tatggggatt ttgaagctca gaggcattgg 240
atggaaatta ctcagcattt atccatagaa aaatggtact tctacgactt gcaatattgg 300
gggcttgact atcctccctt gacagccttt cattcatact tctttggcaa attaggcagc 360
ttcatcaatc cagcatggtt tgctttagac gtctccagag ggtttgaatc agtggatcta 420
aaatcgtaca tgagggcgac cgcaattctc agtgagctgt tatgttttat tccagctgtc 480
atttggtatt gtcgttggat gggacttaac tacttcaatc aaaacgccat tgagcaaact 540
ataatagcgt ctgctattct tttcaatcca tctttaatta tcatagatca tggccacttc 600
cagtacaact cagttatgct aggttttgct ttattatcca tattaaatct gttgtacgat 660
aattttgcat tagcggctat ttttttcgtt ctttcaataa gctttaagca aatggctctc 720
tattatagcc ccatcatgtt tttttacatg ctgagtgtga gttgttggcc tttgaaaaac 780
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ttcccgtttt caagaggctt gtttgaggat aaggtggcca acttttggtg tacaacgaat 960
atactggtaa agtacaaaca gttattcact gacaaaaccc ttactaggat atcgctagta 1020
gcaactttga ttgcaattag tccgtcttgc ttcatcattt ttactcaccc aaagaaggtt 1080
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```
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<210> 77
<211> 547
<212> PRT
<213> Pichia pastoris

<400> 77

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Met Pro His Lys Arg Thr Pro Ser Ser Ser Leu Leu Tyr Ala Arg Ile
  1               5                  10                  15

Pro Gly Ile Ser Phe Glu Asn Ser Pro Val Phe Asp Phe Leu Ser Pro
            20                  25                  30

Phe Gly Pro Ala Pro Asn Gln Trp Val Ala Arg Tyr Ile Ile Ile Ile
        35                  40                  45

Phe Ala Ile Leu Ile Arg Leu Ala Val Gly Leu Gly Ser Tyr Ser Gly
    50                  55                  60

Phe Asn Thr Pro Pro Met Tyr Gly Asp Phe Glu Ala Gln Arg His Trp
65                  70                  75                  80

Met Glu Ile Thr Gln His Leu Ser Ile Glu Lys Trp Tyr Phe Tyr Asp
                85                  90                  95

Leu Gln Tyr Trp Gly Leu Asp Tyr Pro Pro Leu Thr Ala Phe His Ser
            100                 105                 110

Tyr Phe Phe Gly Lys Leu Gly Ser Phe Ile Asn Pro Ala Trp Phe Ala
        115                 120                 125

Leu Asp Val Ser Arg Gly Phe Glu Ser Val Asp Leu Lys Ser Tyr Met
    130                 135                 140

Arg Ala Thr Ala Ile Leu Ser Glu Leu Leu Cys Phe Ile Pro Ala Val
145                 150                 155                 160

Ile Trp Tyr Cys Arg Trp Met Gly Leu Asn Tyr Phe Asn Gln Asn Ala
                165                 170                 175

Ile Glu Gln Thr Ile Ile Ala Ser Ala Ile Leu Phe Asn Pro Ser Leu
            180                 185                 190

Ile Ile Ile Asp His Gly His Phe Gln Tyr Asn Ser Val Met Leu Gly
        195                 200                 205
```

Phe Ala Leu Leu Ser Ile Leu Asn Leu Leu Tyr Asp Asn Phe Ala Leu
210 215 220

Ala Ala Ile Phe Phe Val Leu Ser Ile Ser Phe Lys Gln Met Ala Leu
225 230 235 240

Tyr Tyr Ser Pro Ile Met Phe Phe Tyr Met Leu Ser Val Ser Cys Trp
245 250 255

Pro Leu Lys Asn Phe Asn Leu Leu Arg Leu Ala Thr Ile Ser Ile Ala
260 265 270

Val Leu Leu Thr Phe Ala Thr Leu Leu Leu Pro Phe Val Leu Val Asp
275 280 285

Gly Met Ser Gln Ile Gly Gln Ile Leu Phe Arg Val Phe Pro Phe Ser
290 295 300

Arg Gly Leu Phe Glu Asp Lys Val Ala Asn Phe Trp Cys Thr Thr Asn
305 310 315 320

Ile Leu Val Lys Tyr Lys Gln Leu Phe Thr Asp Lys Thr Leu Thr Arg
325 330 335

Ile Ser Leu Val Ala Thr Leu Ile Ala Ile Ser Pro Ser Cys Phe Ile
340 345 350

Ile Phe Thr His Pro Lys Lys Val Leu Leu Pro Trp Ala Phe Ala Ala
355 360 365

Cys Ser Trp Ala Phe Tyr Leu Phe Ser Phe Gln Val His Glu Lys Ser
370 375 380

Val Leu Val Pro Leu Met Pro Thr Thr Leu Leu Leu Val Glu Lys Asp
385 390 395 400

Leu Asp Ile Ile Ser Met Val Cys Trp Ile Ser Asn Ile Ala Phe Phe
405 410 415

Ser Met Trp Pro Leu Leu Lys Arg Asp Gly Leu Ala Leu Glu Tyr Phe
420 425 430

Val Leu Gly Ile Leu Ser Asn Trp Leu Ile Gly Asn Leu Asn Trp Ile
435 440 445

Ser Lys Trp Leu Val Pro Ser Phe Leu Ile Pro Gly Pro Thr Leu Ser
450 455 460

Lys Lys Val Pro Lys Arg Asp Thr Lys Thr Val Val His Thr His Trp
465 470 475 480

Phe Trp Gly Ser Val Thr Phe Val Ser Tyr Leu Gly Ala Thr Val Ile
485 490 495

Gln Phe Val Asp Trp Leu Tyr Leu Pro Pro Ala Lys Tyr Pro Asp Leu
500 505 510

```
Trp Val Ile Leu Asn Thr Thr Leu Ser Phe Ala Cys Phe Gly Leu Phe
        515                 520                 525

Trp Leu Trp Ile Asn Tyr Asn Leu Tyr Ile Leu Arg Asp Phe Lys Leu
    530                 535                 540

Lys Asp Ala
545
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<210> 78
<211> 527
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (23)..(37)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (366)..(378)
<223> Variable amino acid

<400> 78

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Ser Phe Glu Asn Ser Pro Val Phe Asp Phe Leu Ser Pro Phe Gly Pro
  1               5                  10                  15

Ala Pro Asn Gln Trp Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
             20                  25                  30

Xaa Xaa Xaa Xaa Xaa Val Gly Leu Gly Ser Tyr Ser Gly Phe Asn Thr
         35                  40                  45

Pro Pro Met Tyr Gly Asp Phe Glu Ala Gln Arg His Trp Met Glu Ile
     50                  55                  60

Thr Gln His Leu Ser Ile Glu Lys Trp Tyr Phe Tyr Asp Leu Gln Tyr
 65                  70                  75                  80

Trp Gly Leu Asp Tyr Pro Pro Leu Thr Ala Phe His Ser Tyr Phe Phe
                 85                  90                  95

Gly Lys Leu Gly Ser Phe Ile Asn Pro Ala Trp Phe Ala Leu Asp Val
            100                 105                 110

Ser Arg Gly Phe Glu Ser Val Asp Leu Lys Ser Tyr Met Arg Ala Thr
        115                 120                 125

Ala Ile Leu Ser Glu Leu Leu Cys Phe Ile Pro Ala Val Ile Trp Tyr
    130                 135                 140

Cys Arg Trp Met Gly Leu Asn Tyr Phe Asn Gln Asn Ala Ile Glu Gln
145                 150                 155                 160

Thr Ile Ile Ala Ser Ala Ile Leu Phe Asn Pro Ser Leu Ile Ile Ile
                165                 170                 175
```

```
Asp His Gly His Phe Gln Tyr Asn Ser Val Met Leu Gly Phe Ala Leu
            180                 185                 190

Leu Ser Ile Leu Asn Leu Leu Tyr Asp Asn Phe Ala Leu Ala Ala Ile
        195                 200                 205

Phe Phe Val Leu Ser Ile Ser Phe Lys Gln Met Ala Leu Tyr Tyr Ser
    210                 215                 220

Pro Ile Met Phe Phe Tyr Met Leu Ser Val Ser Cys Trp Pro Leu Lys
225                 230                 235                 240

Asn Phe Asn Leu Leu Arg Leu Ala Thr Ile Ser Ile Ala Val Leu Leu
                245                 250                 255

Thr Phe Ala Thr Leu Leu Leu Pro Phe Val Leu Val Asp Gly Met Ser
            260                 265                 270

Gln Ile Gly Gln Ile Leu Phe Arg Val Phe Pro Phe Ser Arg Gly Leu
        275                 280                 285

Phe Glu Asp Lys Val Ala Asn Phe Trp Cys Thr Thr Asn Ile Leu Val
    290                 295                 300

Lys Tyr Lys Gln Leu Phe Thr Asp Lys Thr Leu Thr Arg Ile Ser Leu
305                 310                 315                 320

Val Ala Thr Leu Ile Ala Ile Ser Pro Ser Cys Phe Ile Ile Phe Thr
            325                 330                 335

His Pro Lys Lys Val Leu Leu Pro Trp Ala Phe Ala Ala Cys Ser Trp
            340                 345                 350

Ala Phe Tyr Leu Phe Ser Phe Gln Val His Glu Lys Ser Xaa Xaa Xaa
        355                 360                 365

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Lys Asp Leu Asp Ile
    370                 375                 380

Ile Ser Met Val Cys Trp Ile Ser Asn Ile Ala Phe Phe Ser Met Trp
385                 390                 395                 400

Pro Leu Leu Lys Arg Asp Gly Leu Ala Leu Glu Tyr Phe Val Leu Gly
                405                 410                 415

Ile Leu Ser Asn Trp Leu Ile Gly Asn Leu Asn Trp Ile Ser Lys Trp
            420                 425                 430

Leu Val Pro Ser Phe Leu Ile Pro Gly Pro Thr Leu Ser Lys Lys Val
        435                 440                 445

Pro Lys Arg Asp Thr Lys Thr Val Val His Thr His Trp Phe Trp Gly
    450                 455                 460

Ser Val Thr Phe Val Ser Tyr Leu Gly Ala Thr Val Ile Gln Phe Val
465                 470                 475                 480
```

```
Asp Trp Leu Tyr Leu Pro Pro Ala Lys Tyr Pro Asp Leu Trp Val Ile
                485                 490                 495

Leu Asn Thr Thr Leu Ser Phe Ala Cys Phe Gly Leu Phe Trp Leu Trp
            500                 505                 510

Ile Asn Tyr Asn Leu Tyr Ile Leu Arg Asp Phe Lys Leu Lys Asp
        515                 520                 525
```

<210> 79
<211> 528
<212> PRT
<213> Saccharomyces cerevisiae

<400> 79

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Ser Phe Tyr Ala Ser Pro Met Tyr Asp Phe Leu Tyr Pro Phe Arg Pro
  1               5                  10                  15

Val Gly Asn Gln Trp Leu Pro Glu Tyr Ile Ile Phe Val Cys Ala Val
            20                  25                  30

Ile Leu Arg Cys Thr Ile Gly Leu Gly Pro Tyr Ser Gly Lys Gly Ser
        35                  40                  45

Pro Pro Leu Tyr Gly Asp Phe Glu Ala Gln Arg His Trp Met Glu Ile
    50                  55                  60

Thr Gln His Leu Pro Leu Ser Lys Trp Tyr Trp Tyr Asp Leu Gln Tyr
65                  70                  75                  80

Trp Gly Leu Asp Tyr Pro Pro Leu Thr Ala Phe His Ser Tyr Leu Leu
                85                  90                  95

Gly Leu Ile Gly Ser Phe Phe Asn Pro Ser Trp Phe Ala Leu Glu Lys
            100                 105                 110

Ser Arg Gly Phe Glu Ser Pro Asp Asn Gly Leu Lys Thr Tyr Met Arg
        115                 120                 125

Ser Thr Val Ile Ile Ser Asp Ile Leu Phe Tyr Phe Pro Ala Val Ile
    130                 135                 140

Tyr Phe Thr Lys Trp Leu Gly Arg Tyr Arg Asn Gln Ser Pro Ile Gly
145                 150                 155                 160

Gln Ser Ile Ala Ala Ser Ala Ile Leu Phe Gln Pro Ser Leu Met Leu
                165                 170                 175

Ile Asp His Gly His Phe Gln Tyr Asn Ser Val Met Leu Gly Leu Thr
            180                 185                 190

Ala Tyr Ala Ile Asn Asn Leu Leu Asp Glu Tyr Tyr Ala Met Ala Ala
        195                 200                 205

Val Cys Phe Val Leu Ser Ile Cys Phe Lys Gln Met Ala Leu Tyr Tyr
    210                 215                 220
```

```
Ala Pro Ile Phe Phe Ala Tyr Leu Leu Ser Arg Ser Leu Leu Phe Pro
225                 230                 235                 240

Lys Phe Asn Ile Ala Arg Leu Thr Val Ile Ala Phe Ala Thr Leu Ala
                245                 250                 255

Thr Phe Ala Ile Ile Phe Ala Pro Leu Tyr Phe Leu Gly Gly Gly Leu
            260                 265                 270

Lys Asn Ile His Gln Cys Ile His Arg Ile Phe Pro Phe Ala Arg Gly
        275                 280                 285

Ile Phe Glu Asp Lys Val Ala Asn Phe Trp Cys Val Thr Asn Val Phe
    290                 295                 300

Val Lys Tyr Lys Glu Arg Phe Thr Ile Gln Gln Leu Gln Leu Tyr Ser
305                 310                 315                 320

Leu Ile Ala Thr Val Ile Gly Phe Leu Pro Ala Met Ile Met Thr Leu
                325                 330                 335

Leu His Pro Lys Lys His Leu Leu Pro Tyr Val Leu Ile Ala Cys Ser
            340                 345                 350

Met Ser Phe Phe Leu Phe Ser Phe Gln Val His Glu Lys Thr Ile Leu
        355                 360                 365

Ile Pro Leu Leu Pro Ile Thr Leu Leu Tyr Ser Ser Thr Asp Trp Asn
    370                 375                 380

Val Leu Ser Leu Val Ser Trp Ile Asn Asn Val Ala Leu Phe Thr Leu
385                 390                 395                 400

Trp Pro Leu Leu Lys Lys Asp Gly Leu His Leu Gln Tyr Ala Val Ser
                405                 410                 415

Phe Leu Leu Ser Asn Trp Leu Ile Gly Asn Phe Ser Phe Ile Thr Pro
            420                 425                 430

Arg Phe Leu Pro Lys Ser Leu Thr Pro Gly Pro Ser Ile Ser Ser Ile
        435                 440                 445

Asn Ser Asp Tyr Arg Arg Arg Ser Leu Leu Pro Tyr Asn Val Val Trp
    450                 455                 460

Lys Ser Phe Ile Ile Gly Thr Tyr Ile Ala Met Gly Phe Tyr His Phe
465                 470                 475                 480

Leu Asp Gln Phe Val Ala Pro Pro Ser Lys Tyr Pro Asp Leu Trp Val
                485                 490                 495

Leu Leu Asn Cys Ala Val Gly Phe Ile Cys Phe Ser Ile Phe Trp Leu
            500                 505                 510

Trp Ser Tyr Tyr Lys Ile Phe Thr Ser Gly Ser Lys Ser Met Lys Asp
        515                 520                 525
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<210> 80
<211> 511
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (22)..(36)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (365)..(379)
<223> Variable amino acid

<400> 80

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Phe Glu Asn Ser Pro Val Phe Asp Phe Leu Ser Pro Phe Gly Pro Ala
  1               5                  10                  15

Pro Asn Gln Trp Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30

Xaa Xaa Xaa Xaa Val Gly Leu Gly Ser Tyr Ser Gly Phe Asn Thr Pro
        35                  40                  45

Pro Met Tyr Gly Asp Phe Glu Ala Gln Arg His Trp Met Glu Ile Thr
    50                  55                  60

Gln His Leu Ser Ile Glu Lys Trp Tyr Phe Tyr Asp Leu Gln Tyr Trp
65                  70                  75                  80

Gly Leu Asp Tyr Pro Pro Leu Thr Ala Phe His Ser Tyr Phe Phe Gly
                85                  90                  95

Lys Leu Gly Ser Phe Ile Asn Pro Ala Trp Phe Ala Leu Asp Val Ser
            100                 105                 110

Arg Gly Phe Glu Ser Val Asp Leu Lys Ser Tyr Met Arg Ala Thr Ala
        115                 120                 125

Ile Leu Ser Glu Leu Leu Cys Phe Ile Pro Ala Val Ile Trp Tyr Cys
    130                 135                 140

Arg Trp Met Gly Leu Asn Tyr Phe Asn Gln Asn Ala Ile Glu Gln Thr
145                 150                 155                 160

Ile Ile Ala Ser Ala Ile Leu Phe Asn Pro Ser Leu Ile Ile Ile Asp
                165                 170                 175

His Gly His Phe Gln Tyr Asn Ser Val Met Leu Gly Phe Ala Leu Leu
            180                 185                 190

Ser Ile Leu Asn Leu Leu Tyr Asp Asn Phe Ala Leu Ala Ala Ile Phe
        195                 200                 205

Phe Val Leu Ser Ile Ser Phe Lys Gln Met Ala Leu Tyr Tyr Ser Pro
    210                 215                 220
```

```
Ile Met Phe Phe Tyr Met Leu Ser Val Ser Cys Trp Pro Leu Lys Asn
225                 230                 235                 240

Phe Asn Leu Leu Arg Leu Ala Thr Ile Ser Ile Ala Val Leu Leu Thr
                245                 250                 255

Phe Ala Thr Leu Leu Leu Pro Phe Val Leu Val Asp Gly Met Ser Gln
            260                 265                 270

Ile Gly Gln Ile Leu Phe Arg Val Phe Pro Phe Ser Arg Gly Leu Phe
        275                 280                 285

Glu Asp Lys Val Ala Asn Phe Trp Cys Thr Thr Asn Ile Leu Val Lys
    290                 295                 300

Tyr Lys Gln Leu Phe Thr Asp Lys Thr Leu Thr Arg Ile Ser Leu Val
305                 310                 315                 320

Ala Thr Leu Ile Ala Ile Ser Pro Ser Cys Phe Ile Ile Phe Thr His
                325                 330                 335

Pro Lys Lys Val Leu Leu Pro Trp Ala Phe Ala Ala Cys Ser Trp Ala
            340                 345                 350

Phe Tyr Leu Phe Ser Phe Gln Val His Glu Lys Ser Xaa Xaa Xaa Xaa
        355                 360                 365

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Lys Asp Leu Asp Ile Ile
    370                 375                 380

Ser Met Val Cys Trp Ile Ser Asn Ile Ala Phe Phe Ser Met Trp Pro
385                 390                 395                 400

Leu Leu Lys Arg Asp Gly Leu Ala Leu Glu Tyr Phe Val Leu Gly Ile
                405                 410                 415

Leu Ser Asn Trp Leu Ile Gly Asn Leu Asn Trp Ile Ser Lys Trp Leu
            420                 425                 430

Val Pro Ser Phe Leu Ile Pro Gly Pro Thr Leu Ser Lys Lys Val Pro
        435                 440                 445

Lys Arg Asp Thr Lys Thr Val Val His Thr His Trp Phe Trp Gly Ser
    450                 455                 460

Val Thr Phe Val Ser Tyr Leu Gly Ala Thr Val Ile Gln Phe Val Asp
465                 470                 475                 480

Trp Leu Tyr Leu Pro Pro Ala Lys Tyr Pro Asp Leu Trp Val Ile Leu
                485                 490                 495

Asn Thr Thr Leu Ser Phe Ala Cys Phe Gly Leu Phe Trp Leu Trp
            500                 505                 510
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<210> 81
<211> 480

<212> PRT
<213> Schizosaccharomyces pombe

<400> 81

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Phe Glu Asn Gly Ala Pro Val Gln Gln Phe Val Ser Arg Phe Arg Ser
  1               5                  10                  15

Tyr Ser Ser Lys Phe Leu Phe Phe Pro Cys Leu Ile Met Ser Leu Val
             20                  25                  30

Phe Met Gln Trp Leu Ile Ser Ile Gly Pro Tyr Ser Gly Tyr Asn Thr
         35                  40                  45

Pro Pro Met Tyr Gly Asp Phe Glu Ala Gln Arg His Trp Met Glu Leu
     50                  55                  60

Thr Leu His Thr Pro Val Ser Gln Trp Tyr Phe Arg Asp Leu Gln Trp
 65                  70                  75                  80

Trp Gly Leu Asp Tyr Pro Pro Leu Thr Ala Tyr Val Ser Trp Phe Phe
                 85                  90                  95

Gly Ile Ile Gly His Tyr Phe Phe Asn Pro Glu Trp Phe Ala Asp Val
            100                 105                 110

Thr Ser Arg Gly Phe Glu Ser Leu Glu Leu Lys Leu Phe Met Arg Ser
        115                 120                 125

Thr Val Ile Ala Ser His Leu Leu Ile Leu Val Pro Pro Leu Met Phe
    130                 135                 140

Tyr Ser Lys Trp Trp Ser Arg Arg Ile Pro Asn Phe Val Asp Arg Asn
145                 150                 155                 160

Ala Ser Leu Ile Met Val Leu Phe Gln Pro Ala Leu Leu Leu Ile Asp
                165                 170                 175

His Gly His Phe Gln Tyr Asn Cys Val Met Leu Gly Leu Val Met Tyr
            180                 185                 190

Ala Ile Ala Asn Leu Leu Lys Asn Gln Tyr Val Ala Ala Thr Phe Phe
        195                 200                 205

Phe Cys Leu Ala Leu Thr Phe Lys Gln Met Ala Leu Tyr Phe Ala Pro
    210                 215                 220

Pro Ile Phe Phe Tyr Leu Leu Gly Thr Cys Val Lys Pro Lys Ile Arg
225                 230                 235                 240

Phe Ser Arg Phe Ile Leu Leu Ser Val Thr Val Val Phe Thr Phe Ser
                245                 250                 255

Leu Ile Leu Phe Pro Trp Ile Tyr Met Asp Tyr Lys Thr Leu Leu Pro
            260                 265                 270

Gln Ile Leu His Arg Val Phe Pro Phe Ala Arg Gly Leu Trp Glu Asp
        275                 280                 285
```

```
Lys Val Ala Asn Phe Trp Cys Thr Leu Asn Thr Val Phe Lys Ile Arg
    290                 295                 300

Glu Val Phe Thr Leu His Gln Leu Gln Val Ile Ser Leu Ile Phe Thr
305                 310                 315                 320

Leu Ile Ser Ile Leu Pro Ser Cys Val Ile Leu Phe Leu Tyr Pro Arg
                325                 330                 335

Lys Arg Leu Leu Ala Leu Gly Phe Ala Ser Ala Ser Trp Gly Phe Phe
            340                 345                 350

Leu Phe Ser Phe Gln Val His Glu Lys Ser Val Leu Leu Pro Leu Leu
        355                 360                 365

Pro Thr Ser Ile Leu Leu Cys His Gly Asn Ile Thr Thr Lys Pro Trp
    370                 375                 380

Ile Ala Leu Ala Asn Asn Leu Ala Val Phe Ser Leu Trp Pro Leu Leu
385                 390                 395                 400

Lys Lys Asp Gly Leu Gly Leu Gln Tyr Phe Thr Leu Val Leu Met Trp
                405                 410                 415

Asn Trp Ile Gly Asp Met Val Val Phe Ser Lys Asn Val Leu Phe Arg
            420                 425                 430

Phe Ile Gln Leu Ser Phe Tyr Val Gly Met Ile Val Ile Leu Gly Ile
        435                 440                 445

Asp Leu Phe Ile Pro Pro Pro Ser Arg Tyr Pro Asp Leu Trp Val Ile
    450                 455                 460

Leu Asn Val Thr Leu Ser Phe Ala Gly Phe Phe Thr Ile Tyr Leu Trp
465                 470                 475                 480


<210> 82
<211> 477
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (329)..(341)
<223> Variable amino acid

<400> 82
Val Gly Leu Gly Ser Tyr Ser Gly Phe Asn Thr Pro Pro Met Tyr Gly
  1               5                  10                  15

Asp Phe Glu Ala Gln Arg His Trp Met Glu Ile Thr Gln His Leu Ser
             20                  25                  30

Ile Glu Lys Trp Tyr Phe Tyr Asp Leu Gln Tyr Trp Gly Leu Asp Tyr
         35                  40                  45
```

```
Pro Pro Leu Thr Ala Phe His Ser Tyr Phe Phe Gly Lys Leu Gly Ser
     50                  55                  60

Phe Ile Asn Pro Ala Trp Phe Ala Leu Asp Val Ser Arg Gly Phe Glu
 65                  70                  75                  80

Ser Val Asp Leu Lys Ser Tyr Met Arg Ala Thr Ala Ile Leu Ser Glu
                 85                  90                  95

Leu Leu Cys Phe Ile Pro Ala Val Ile Trp Tyr Cys Arg Trp Met Gly
            100                 105                 110

Leu Asn Tyr Phe Asn Gln Asn Ala Ile Glu Gln Thr Ile Ile Ala Ser
        115                 120                 125

Ala Ile Leu Phe Asn Pro Ser Leu Ile Ile Ile Asp His Gly His Phe
    130                 135                 140

Gln Tyr Asn Ser Val Met Leu Gly Phe Ala Leu Leu Ser Ile Leu Asn
145                 150                 155                 160

Leu Leu Tyr Asp Asn Phe Ala Leu Ala Ala Ile Phe Phe Val Leu Ser
                165                 170                 175

Ile Ser Phe Lys Gln Met Ala Leu Tyr Tyr Ser Pro Ile Met Phe Phe
            180                 185                 190

Tyr Met Leu Ser Val Ser Cys Trp Pro Leu Lys Asn Phe Asn Leu Leu
        195                 200                 205

Arg Leu Ala Thr Ile Ser Ile Ala Val Leu Leu Thr Phe Ala Thr Leu
    210                 215                 220

Leu Leu Pro Phe Val Leu Val Asp Gly Met Ser Gln Ile Gly Gln Ile
225                 230                 235                 240

Leu Phe Arg Val Phe Pro Phe Ser Arg Gly Leu Phe Glu Asp Lys Val
                245                 250                 255

Ala Asn Phe Trp Cys Thr Thr Asn Ile Leu Val Lys Tyr Lys Gln Leu
            260                 265                 270

Phe Thr Asp Lys Thr Leu Thr Arg Ile Ser Leu Val Ala Thr Leu Ile
        275                 280                 285

Ala Ile Ser Pro Ser Cys Phe Ile Ile Phe Thr His Pro Lys Lys Val
    290                 295                 300

Leu Leu Pro Trp Ala Phe Ala Ala Cys Ser Trp Ala Phe Tyr Leu Phe
305                 310                 315                 320

Ser Phe Gln Val His Glu Lys Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                325                 330                 335

Xaa Xaa Xaa Xaa Xaa Glu Lys Asp Leu Asp Ile Ile Ser Met Val Cys
            340                 345                 350
```

```
Trp Ile Ser Asn Ile Ala Phe Phe Ser Met Trp Pro Leu Leu Lys Arg
        355                 360                 365

Asp Gly Leu Ala Leu Glu Tyr Phe Val Leu Gly Ile Leu Ser Asn Trp
    370                 375                 380

Leu Ile Gly Asn Leu Asn Trp Ile Ser Lys Trp Leu Val Pro Ser Phe
385                 390                 395                 400

Leu Ile Pro Gly Pro Thr Leu Ser Lys Lys Val Pro Lys Arg Asp Thr
                405                 410                 415

Lys Thr Val Val His Thr His Trp Phe Trp Gly Ser Val Thr Phe Val
            420                 425                 430

Ser Tyr Leu Gly Ala Thr Val Ile Gln Phe Val Asp Trp Leu Tyr Leu
        435                 440                 445

Pro Pro Ala Lys Tyr Pro Asp Leu Trp Val Ile Leu Asn Thr Thr Leu
    450                 455                 460

Ser Phe Ala Cys Phe Gly Leu Phe Trp Leu Trp Ile Asn
465                 470                 475


<210> 83
<211> 448
<212> PRT
<213> Drosophila melanogaster

<400> 83
Ile Ser Leu Tyr Ser Tyr Ser Gly Phe Asp Ser Pro Pro Met His Gly
  1               5                  10                  15

Asp Tyr Glu Ala Gln Arg His Trp Gln Glu Ile Thr Val Asn Leu Ala
            20                  25                  30

Val Gly Glu Trp Tyr Thr Asn Ser Ser Asn Asn Asp Leu Gln Tyr Trp
        35                  40                  45

Gly Leu Asp Tyr Pro Pro Leu Thr Ala Tyr His Ser Tyr Leu Val Gly
    50                  55                  60

Arg Ile Gly Ala Ser Ile Asp Pro Arg Phe Val Glu Leu His Lys Ser
65                  70                  75                  80

Arg Gly Phe Glu Ser Lys Glu His Lys Arg Phe Met Arg Ala Thr Val
                85                  90                  95

Val Ser Ala Asp Val Leu Ile Tyr Leu Pro Ala Met Leu Leu Leu Ala
            100                 105                 110

Tyr Ser Leu Asp Lys Ala Phe Arg Ser Asp Asp Lys Leu Phe Leu Phe
        115                 120                 125

Thr Leu Val Ala Ala Tyr Pro Gly Gln Thr Leu Ile Asp Asn Gly His
    130                 135                 140
```

```
Phe Gln Tyr Asn Asn Ile Ser Leu Gly Phe Ala Ala Val Ala Ile Ala
145                 150                 155                 160

Ala Ile Leu Arg Arg Arg Phe Tyr Ala Ala Ala Phe Phe Phe Thr Leu
                165                 170                 175

Ala Leu Asn Tyr Lys Gln Met Glu Leu Tyr His Ser Leu Pro Phe Phe
            180                 185                 190

Ala Phe Leu Leu Gly Glu Cys Val Ser Gln Lys Ser Phe Ala Ser Phe
        195                 200                 205

Ile Ala Glu Ile Ser Arg Ile Ala Ala Val Val Leu Gly Thr Phe Ala
    210                 215                 220

Ile Leu Trp Val Pro Trp Leu Gly Ser Leu Gln Ala Val Leu Gln Val
225                 230                 235                 240

Leu His Arg Leu Phe Pro Val Ala Arg Gly Val Phe Glu Asp Lys Val
                245                 250                 255

Ala Asn Val Trp Cys Ala Val Asn Val Val Trp Lys Leu Lys Lys His
            260                 265                 270

Ile Ser Asn Asp Gln Met Ala Leu Val Cys Ile Ala Cys Thr Leu Ile
        275                 280                 285

Ala Ser Leu Pro Thr Asn Val Leu Leu Phe Arg Arg Arg Thr Asn Val
    290                 295                 300

Gly Phe Leu Leu Ala Leu Phe Asn Thr Ser Leu Ala Phe Phe Leu Phe
305                 310                 315                 320

Ser Phe Gln Val His Glu Lys Thr Ile Leu Leu Thr Ala Leu Pro Ala
                325                 330                 335

Leu Phe Leu Leu Lys Cys Trp Pro Asp Glu Met Ile Leu Phe Leu Glu
            340                 345                 350

Val Thr Val Phe Ser Met Leu Pro Leu Leu Ala Arg Asp Glu Leu Leu
        355                 360                 365

Val Pro Ala Val Val Ala Thr Val Ala Phe His Leu Ile Phe Lys Cys
    370                 375                 380

Phe Asp Ser Lys Ser Lys Leu Ser Asn Glu Tyr Pro Leu Lys Tyr Ile
385                 390                 395                 400

Ala Asn Ile Ser Gln Ile Leu Met Ile Ser Val Val Val Ala Ser Leu
                405                 410                 415

Thr Val Pro Ala Pro Thr Lys Tyr Pro Asp Leu Trp Pro Leu Ile Ile
            420                 425                 430

Ser Val Thr Ser Cys Gly His Phe Phe Leu Phe Phe Leu Trp Gly Asn
        435                 440                 445
```

<210> 84
<211> 478
<212> PRT
<213> Pichia pastoris

<220>
<221> MOD_RES
<222> (324)..(336)
<223> Variable amino acid

<400> 84

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Tyr Ser Gly Phe Asn Thr Pro Pro Met Tyr Gly Asp Phe Glu Ala Gln
  1               5                  10                  15

Arg His Trp Met Glu Ile Thr Gln His Leu Ser Ile Glu Lys Trp Tyr
             20                  25                  30

Phe Tyr Asp Leu Gln Tyr Trp Gly Leu Asp Tyr Pro Pro Leu Thr Ala
         35                  40                  45

Phe His Ser Tyr Phe Phe Gly Lys Leu Gly Ser Phe Ile Asn Pro Ala
     50                  55                  60

Trp Phe Ala Leu Asp Val Ser Arg Gly Phe Glu Ser Val Asp Leu Lys
 65                  70                  75                  80

Ser Tyr Met Arg Ala Thr Ala Ile Leu Ser Glu Leu Leu Cys Phe Ile
                 85                  90                  95

Pro Ala Val Ile Trp Tyr Cys Arg Trp Met Gly Leu Asn Tyr Phe Asn
            100                 105                 110

Gln Asn Ala Ile Glu Gln Thr Ile Ile Ala Ser Ala Ile Leu Phe Asn
        115                 120                 125

Pro Ser Leu Ile Ile Ile Asp His Gly His Phe Gln Tyr Asn Ser Val
    130                 135                 140

Met Leu Gly Phe Ala Leu Leu Ser Ile Leu Asn Leu Leu Tyr Asp Asn
145                 150                 155                 160

Phe Ala Leu Ala Ala Ile Phe Phe Val Leu Ser Ile Ser Phe Lys Gln
                165                 170                 175

Met Ala Leu Tyr Tyr Ser Pro Ile Met Phe Phe Tyr Met Leu Ser Val
            180                 185                 190

Ser Cys Trp Pro Leu Lys Asn Phe Asn Leu Leu Arg Leu Ala Thr Ile
        195                 200                 205

Ser Ile Ala Val Leu Leu Thr Phe Ala Thr Leu Leu Leu Pro Phe Val
    210                 215                 220

Leu Val Asp Gly Met Ser Gln Ile Gly Gln Ile Leu Phe Arg Val Phe
225                 230                 235                 240

Pro Phe Ser Arg Gly Leu Phe Glu Asp Lys Val Ala Asn Phe Trp Cys
                245                 250                 255
```

```
Thr Thr Asn Ile Leu Val Lys Tyr Lys Gln Leu Phe Thr Asp Lys Thr
            260                 265                 270

Leu Thr Arg Ile Ser Leu Val Ala Thr Leu Ile Ala Ile Ser Pro Ser
        275                 280                 285

Cys Phe Ile Ile Phe Thr His Pro Lys Lys Val Leu Leu Pro Trp Ala
    290                 295                 300

Phe Ala Ala Cys Ser Trp Ala Phe Tyr Leu Phe Ser Phe Gln Val His
305                 310                 315                 320

Glu Lys Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                325                 330                 335

Glu Lys Asp Leu Asp Ile Ile Ser Met Val Cys Trp Ile Ser Asn Ile
            340                 345                 350

Ala Phe Phe Ser Met Trp Pro Leu Leu Lys Arg Asp Gly Leu Ala Leu
        355                 360                 365

Glu Tyr Phe Val Leu Gly Ile Leu Ser Asn Trp Leu Ile Gly Asn Leu
    370                 375                 380

Asn Trp Ile Ser Lys Trp Leu Val Pro Ser Phe Leu Ile Pro Gly Pro
385                 390                 395                 400

Thr Leu Ser Lys Lys Val Pro Lys Arg Asp Thr Lys Thr Val Val His
            405                 410                 415

Thr His Trp Phe Trp Gly Ser Val Thr Phe Val Ser Tyr Leu Gly Ala
            420                 425                 430

Thr Val Ile Gln Phe Val Asp Trp Leu Tyr Leu Pro Pro Ala Lys Tyr
        435                 440                 445

Pro Asp Leu Trp Val Ile Leu Asn Thr Thr Leu Ser Phe Ala Cys Phe
    450                 455                 460

Gly Leu Phe Trp Leu Trp Ile Asn Tyr Asn Leu Tyr Ile Leu
465                 470                 475


<210> 85
<211> 459
<212> PRT
<213> Arabidopsis thaliana

<400> 85
Tyr Ser Gly Ala Gly Ile Pro Pro Lys Phe Gly Asp Phe Glu Ala Gln
  1               5                  10                  15

Arg His Trp Met Glu Ile Thr Thr Asn Leu Pro Val Ile Asp Trp Tyr
             20                  25                  30

Arg Asn Gly Thr Tyr Asn Asp Leu Thr Tyr Trp Gly Leu Asp Tyr Pro
         35                  40                  45
```

```
Pro Leu Thr Ala Tyr Gln Ser Tyr Ile His Gly Ile Phe Leu Arg Phe
     50                  55                  60

Phe Asn Pro Glu Ser Val Ala Leu Leu Ser Ser Arg Gly His Glu Ser
 65                  70                  75                  80

Tyr Leu Gly Lys Leu Leu Met Arg Trp Thr Val Leu Ser Ser Asp Ala
                 85                  90                  95

Phe Ile Phe Phe Pro Ala Ala Leu Phe Phe Val Leu Val Tyr His Arg
            100                 105                 110

Asn Arg Thr Arg Gly Gly Lys Ser Glu Val Ala Trp His Ile Ala Met
        115                 120                 125

Ile Leu Leu Asn Pro Cys Leu Ile Leu Ile Asp His Gly His Phe Gln
    130                 135                 140

Tyr Asn Cys Ile Ser Leu Gly Leu Thr Val Gly Ala Ile Ala Ala Val
145                 150                 155                 160

Leu Cys Glu Ser Glu Val Leu Thr Cys Val Leu Phe Ser Leu Ala Leu
                165                 170                 175

Ser His Lys Gln Met Ser Ala Tyr Phe Ala Pro Ala Phe Phe Ser His
            180                 185                 190

Leu Leu Gly Lys Cys Leu Arg Arg Lys Ser Pro Ile Leu Ser Val Ile
        195                 200                 205

Lys Leu Gly Ile Ala Val Ile Val Thr Phe Val Ile Phe Trp Trp Pro
    210                 215                 220

Tyr Val His Ser Leu Asp Asp Phe Leu Met Val Leu Ser Arg Leu Ala
225                 230                 235                 240

Pro Phe Glu Arg Gly Ile Tyr Glu Asp Tyr Val Ala Asn Phe Trp Cys
                245                 250                 255

Thr Thr Ser Ile Leu Ile Lys Trp Lys Asn Leu Phe Thr Thr Gln Ser
            260                 265                 270

Leu Lys Ser Ile Ser Leu Ala Ala Thr Ile Leu Ala Ser Leu Pro Ser
        275                 280                 285

Met Val Gln Gln Ile Leu Ser Pro Ser Asn Glu Gly Phe Leu Tyr Gly
    290                 295                 300

Leu Leu Asn Ser Ser Met Ala Phe Tyr Leu Phe Ser Phe Gln Val His
305                 310                 315                 320

Glu Lys Ser Ile Leu Met Pro Phe Leu Ser Ala Thr Leu Leu Ala Leu
                325                 330                 335

Lys Leu Pro Asp His Phe Ser His Leu Thr Tyr Tyr Ala Leu Phe Ser
            340                 345                 350
```

```
Met Phe Pro Leu Leu Cys Arg Asp Lys Leu Leu Ile Pro Tyr Leu Thr
        355                 360                 365

Leu Ser Phe Leu Phe Thr Val Ile Tyr His Ser Pro Gly Asn His His
    370                 375                 380

Ala Ile Gln Lys Thr Asp Val Ser Phe Phe Ser Phe Lys Asn Phe Pro
385                 390                 395                 400

Gly Tyr Val Phe Leu Leu Arg Thr His Phe Phe Ile Ser Val Val Leu
                405                 410                 415

His Val Leu Tyr Leu Thr Ile Lys Pro Pro Gln Lys Tyr Pro Phe Leu
            420                 425                 430

Phe Glu Ala Leu Ile Met Ile Leu Cys Phe Ser Tyr Phe Ile Met Phe
        435                 440                 445

Ala Phe Tyr Thr Asn Tyr Thr Gln Trp Thr Leu
    450                 455
```

<210> 86
<211> 836
<212> DNA
<213> Kluyveromyces lactis

<400> 86
atctctgttt caacagctct tgcattcatt ggttctttcg gtccaatcta tatctttgga 60
ggatacaaga acttagtgca atcaatgcac aggatttttc catttgccag gggtatcttt 120
gaagataaag ttgcgaattt ttggtgcgtt tctaatattt tcatcaaata tagaaatcta 180
ttcactcaga aggatcttca attatactca ttactcgcaa cagttattgg gcttttacca 240
tcattcatta taacattttt atacccgaag agacatttac taccatatgc tttggccgca 300
tgttcgatgt cattcttctt attcagcttc caggttcatg aaaagacaat cttattacct 360
ttacttccta ttacactctt gtacacgtca agagattgga atgttctatc attggtttgt 420
tggattaaca acgtggcatt gtttacactc tggccattac tgaaaaagga caatctagta 480
ttgcaatatg gagtcatgtt catgtttagc aattggttga tcggtaactt cagtttcgtc 540
acaccacgct tcctcccaaa atttttgaca ccagggccat ccatcagtga tatagatgtt 600
gattatagac gggcaagttt actacccaag agcctaatat ggagattaat cattgttggc 660
tcatatattg caatggggat tattcatttt ctagactatt acgtctcccc gccatcaaaa 720
taccctgatt tatgggtgct tgccaattgt tccttgggct tctcatgttt tgtgacattt 780
tggatatgga acaattataa ttattcgaaa tgagaaacag cactttgcaa gattta 836

<210> 87
<211> 277
<212> PRT
<213> Kluyveromyces lactis

<400> 87
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Ile Ser Val Ser Thr Ala Leu Ala Phe Ile Gly Ser Phe Gly Pro Ile
  1               5                  10                  15

Tyr Ile Phe Gly Gly Tyr Lys Asn Leu Val Gln Ser Met His Arg Ile
            20                  25                  30

Phe Pro Phe Ala Arg Gly Ile Phe Glu Asp Lys Val Ala Asn Phe Trp
        35                  40                  45
```

```
Cys Val Ser Asn Ile Phe Ile Lys Tyr Arg Asn Leu Phe Thr Gln Lys
     50                  55                  60

Asp Leu Gln Leu Tyr Ser Leu Leu Ala Thr Val Ile Gly Leu Leu Pro
 65                  70                  75                  80

Ser Phe Ile Ile Thr Phe Leu Tyr Pro Lys Arg His Leu Leu Pro Tyr
                85                  90                  95

Ala Leu Ala Ala Cys Ser Met Ser Phe Phe Leu Phe Ser Phe Gln Val
            100                 105                 110

His Glu Lys Thr Ile Leu Leu Pro Leu Leu Pro Ile Thr Leu Leu Tyr
        115                 120                 125

Thr Ser Arg Asp Trp Asn Val Leu Ser Leu Val Cys Trp Ile Asn Asn
    130                 135                 140

Val Ala Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys Asp Asn Leu Val
145                 150                 155                 160

Leu Gln Tyr Gly Val Met Phe Met Phe Ser Asn Trp Leu Ile Gly Asn
                165                 170                 175

Phe Ser Phe Val Thr Pro Arg Phe Leu Pro Lys Phe Leu Thr Pro Gly
            180                 185                 190

Pro Ser Ile Ser Asp Ile Asp Val Asp Tyr Arg Arg Ala Ser Leu Leu
        195                 200                 205

Pro Lys Ser Leu Ile Trp Arg Leu Ile Ile Val Gly Ser Tyr Ile Ala
    210                 215                 220

Met Gly Ile Ile His Phe Leu Asp Tyr Tyr Val Ser Pro Pro Ser Lys
225                 230                 235                 240

Tyr Pro Asp Leu Trp Val Leu Ala Asn Cys Ser Leu Gly Phe Ser Cys
                245                 250                 255

Phe Val Thr Phe Trp Ile Trp Asn Asn Tyr Asn Tyr Ser Lys Glu Thr
            260                 265                 270

Ala Leu Cys Lys Ile
        275
```

<210> 88
<211> 284
<212> PRT
<213> Kluyveromyces lactis

<220>
<221> MOD_RES
<222> (116)..(127)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (271)
<223> Variable amino acid

<400> 88

```
Ile Ser Val Ser Thr Ala Leu Ala Phe Ile Gly Ser Phe Gly Pro Ile
  1               5                  10                  15

Tyr Ile Phe Gly Gly Tyr Lys Asn Leu Val Gln Ser Met His Arg Ile
             20                  25                  30

Phe Pro Phe Ala Arg Gly Ile Phe Glu Asp Lys Val Ala Asn Phe Trp
         35                  40                  45

Cys Val Ser Asn Ile Phe Ile Lys Tyr Arg Asn Leu Phe Thr Gln Lys
     50                  55                  60

Asp Leu Gln Leu Tyr Ser Leu Leu Ala Thr Val Ile Gly Leu Leu Pro
 65                  70                  75                  80

Ser Phe Ile Ile Thr Phe Leu Tyr Pro Lys Arg His Leu Leu Pro Tyr
                 85                  90                  95

Ala Leu Ala Ala Cys Ser Met Ser Phe Phe Leu Phe Ser Phe Gln Val
            100                 105                 110

His Glu Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
        115                 120                 125

Thr Ser Arg Asp Trp Asn Val Leu Ser Leu Val Cys Trp Ile Asn Asn
    130                 135                 140

Val Ala Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys Asp Asn Leu Val
145                 150                 155                 160

Leu Gln Tyr Gly Val Met Phe Met Phe Ser Asn Trp Leu Ile Gly Asn
                165                 170                 175

Phe Ser Phe Val Thr Pro Arg Phe Leu Pro Lys Phe Leu Thr Pro Gly
            180                 185                 190

Pro Ser Ile Ser Asp Ile Asp Val Asp Tyr Arg Arg Ala Ser Leu Leu
        195                 200                 205

Pro Lys Ser Leu Ile Trp Arg Leu Ile Ile Val Gly Ser Tyr Ile Ala
    210                 215                 220

Met Gly Ile Ile His Phe Leu Asp Tyr Tyr Val Ser Pro Pro Ser Gln
225                 230                 235                 240

Glu Arg Tyr Lys Tyr Pro Asp Leu Trp Val Leu Ala Asn Cys Ser Leu
                245                 250                 255

Gly Phe Ser Cys Phe Val Thr Phe Trp Ile Trp Asn Asn Tyr Xaa Leu
            260                 265                 270
```

```
Phe Glu Arg Met Arg Asn Ser Thr Leu Gln Asp Leu
        275                 280


<210> 89
<211> 280
<212> PRT
<213> Saccharomyces cerevisiae

<400> 89
Ile Ala Phe Ala Thr Leu Ala Thr Phe Ala Ile Ile Phe Ala Pro Leu
  1               5                  10                  15

Tyr Phe Leu Gly Gly Gly Leu Lys Asn Ile His Gln Cys Ile His Arg
             20                  25                  30

Ile Phe Pro Phe Ala Arg Gly Ile Phe Glu Asp Lys Val Ala Asn Phe
         35                  40                  45

Trp Cys Val Thr Asn Val Phe Val Lys Tyr Lys Glu Arg Phe Thr Ile
     50                  55                  60

Gln Gln Leu Gln Leu Tyr Ser Leu Ile Ala Thr Val Ile Gly Phe Leu
 65                  70                  75                  80

Pro Ala Met Ile Met Thr Leu Leu His Pro Lys Lys His Leu Leu Pro
                 85                  90                  95

Tyr Val Leu Ile Ala Cys Ser Met Ser Phe Phe Leu Phe Ser Phe Gln
            100                 105                 110

Val His Glu Lys Thr Ile Leu Ile Pro Leu Leu Pro Ile Thr Leu Leu
        115                 120                 125

Tyr Ser Ser Thr Asp Trp Asn Val Leu Ser Leu Val Ser Trp Ile Asn
    130                 135                 140

Asn Val Ala Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys Asp Gly Leu
145                 150                 155                 160

His Leu Gln Tyr Ala Val Ser Phe Leu Leu Ser Asn Trp Leu Ile Gly
                165                 170                 175

Asn Phe Ser Phe Ile Thr Pro Arg Phe Leu Pro Lys Ser Leu Thr Pro
            180                 185                 190

Gly Pro Ser Ile Ser Ser Ile Asn Ser Asp Tyr Arg Arg Arg Ser Leu
        195                 200                 205

Leu Pro Tyr Asn Val Val Trp Lys Ser Phe Ile Ile Gly Thr Tyr Ile
    210                 215                 220

Ala Met Gly Phe Tyr His Phe Leu Asp Gln Phe Val Ala Pro Pro Ser
225                 230                 235                 240

Lys Tyr Pro Asp Leu Trp Val Leu Leu Asn Cys Ala Val Gly Phe Ile
                245                 250                 255
```

```
Cys Phe Ser Ile Phe Trp Leu Trp Ser Tyr Tyr Lys Ile Phe Thr Ser
            260                 265                 270

Gly Ser Lys Ser Met Lys Asp Leu
        275                 280


<210> 90
<211> 284
<212> PRT
<213> Kluyveromyces lactis

<220>
<221> MOD_RES
<222> (116)..(127)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (271)
<223> Variable amino acid

<400> 90
Ile Ser Val Ser Thr Ala Leu Ala Phe Ile Gly Ser Phe Gly Pro Ile
  1               5                  10                  15

Tyr Ile Phe Gly Gly Tyr Lys Asn Leu Val Gln Ser Met His Arg Ile
             20                  25                  30

Phe Pro Phe Ala Arg Gly Ile Phe Glu Asp Lys Val Ala Asn Phe Trp
         35                  40                  45

Cys Val Ser Asn Ile Phe Ile Lys Tyr Arg Asn Leu Phe Thr Gln Lys
     50                  55                  60

Asp Leu Gln Leu Tyr Ser Leu Leu Ala Thr Val Ile Gly Leu Leu Pro
 65                  70                  75                  80

Ser Phe Ile Ile Thr Phe Leu Tyr Pro Lys Arg His Leu Leu Pro Tyr
                 85                  90                  95

Ala Leu Ala Ala Cys Ser Met Ser Phe Phe Leu Phe Ser Phe Gln Val
            100                 105                 110

His Glu Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
        115                 120                 125

Thr Ser Arg Asp Trp Asn Val Leu Ser Leu Val Cys Trp Ile Asn Asn
    130                 135                 140

Val Ala Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys Asp Asn Leu Val
145                 150                 155                 160

Leu Gln Tyr Gly Val Met Phe Met Phe Ser Asn Trp Leu Ile Gly Asn
                165                 170                 175

Phe Ser Phe Val Thr Pro Arg Phe Leu Pro Lys Phe Leu Thr Pro Gly
            180                 185                 190
```

```
Pro Ser Ile Ser Asp Ile Asp Val Asp Tyr Arg Arg Ala Ser Leu Leu
        195                 200                 205

Pro Lys Ser Leu Ile Trp Arg Leu Ile Ile Val Gly Ser Tyr Ile Ala
    210                 215                 220

Met Gly Ile Ile His Phe Leu Asp Tyr Tyr Val Ser Pro Pro Ser Gln
225                 230                 235                 240

Glu Arg Tyr Lys Tyr Pro Asp Leu Trp Val Leu Ala Asn Cys Ser Leu
                245                 250                 255

Gly Phe Ser Cys Phe Val Thr Phe Trp Ile Trp Asn Asn Tyr Xaa Leu
            260                 265                 270

Phe Glu Arg Met Arg Asn Ser Thr Leu Gln Asp Leu
        275                 280


<210> 91
<211> 250
<212> PRT
<213> Schizosaccharomyces pombe

<400> 91
Leu Ser Val Thr Val Val Phe Thr Phe Ser Leu Ile Leu Phe Pro Trp
  1               5                  10                  15

Ile Tyr Met Asp Tyr Lys Thr Leu Leu Pro Gln Ile Leu His Arg Val
            20                  25                  30

Phe Pro Phe Ala Arg Gly Leu Trp Glu Asp Lys Val Ala Asn Phe Trp
        35                  40                  45

Cys Thr Leu Asn Thr Val Phe Lys Ile Arg Glu Val Phe Thr Leu His
    50                  55                  60

Gln Leu Gln Val Ile Ser Leu Ile Phe Thr Leu Ile Ser Ile Leu Pro
65                  70                  75                  80

Ser Cys Val Ile Leu Phe Leu Tyr Pro Arg Lys Arg Leu Leu Ala Leu
                85                  90                  95

Gly Phe Ala Ser Ala Ser Trp Gly Phe Phe Leu Phe Ser Phe Gln Val
            100                 105                 110

His Glu Lys Ser Val Leu Leu Pro Leu Leu Pro Thr Ser Ile Leu Leu
        115                 120                 125

Cys His Gly Asn Ile Thr Thr Lys Pro Trp Ile Ala Leu Ala Asn Asn
    130                 135                 140

Leu Ala Val Phe Ser Leu Trp Pro Leu Leu Lys Lys Asp Gly Leu Gly
145                 150                 155                 160

Leu Gln Tyr Phe Thr Leu Val Leu Met Trp Asn Trp Ile Gly Asp Met
                165                 170                 175
```

```
Val Val Phe Ser Lys Asn Val Leu Phe Arg Phe Ile Gln Leu Ser Phe
            180                 185                 190

Tyr Val Gly Met Ile Val Ile Leu Gly Ile Asp Leu Phe Ile Pro Pro
        195                 200                 205

Pro Ser Arg Tyr Pro Asp Leu Trp Val Ile Leu Asn Val Thr Leu Ser
    210                 215                 220

Phe Ala Gly Phe Phe Thr Ile Tyr Leu Trp Thr Leu Gly Arg Leu Leu
225                 230                 235                 240

His Ile Ser Ser Lys Leu Ser Thr Asp Leu
                245                 250
```

<210> 92
<211> 238
<212> PRT
<213> Kluyveromyces lactis

<220>
<221> MOD_RES
<222> (88)..(99)
<223> Variable amino acid

<400> 92

```
Met His Arg Ile Phe Pro Phe Ala Arg Gly Ile Phe Glu Asp Lys Val
  1               5                  10                  15

Ala Asn Phe Trp Cys Val Ser Asn Ile Phe Ile Lys Tyr Arg Asn Leu
            20                  25                  30

Phe Thr Gln Lys Asp Leu Gln Leu Tyr Ser Leu Leu Ala Thr Val Ile
        35                  40                  45

Gly Leu Leu Pro Ser Phe Ile Ile Thr Phe Leu Tyr Pro Lys Arg His
    50                  55                  60

Leu Leu Pro Tyr Ala Leu Ala Ala Cys Ser Met Ser Phe Phe Leu Phe
65                  70                  75                  80

Ser Phe Gln Val His Glu Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85                  90                  95

Xaa Xaa Xaa Tyr Thr Ser Arg Asp Trp Asn Val Leu Ser Leu Val Cys
            100                 105                 110

Trp Ile Asn Asn Val Ala Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys
        115                 120                 125

Asp Asn Leu Val Leu Gln Tyr Gly Val Met Phe Met Phe Ser Asn Trp
    130                 135                 140

Leu Ile Gly Asn Phe Ser Phe Val Thr Pro Arg Phe Leu Pro Lys Phe
145                 150                 155                 160
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```
Leu Thr Pro Gly Pro Ser Ile Ser Asp Ile Asp Val Asp Tyr Arg Arg
                165                 170                 175

Ala Ser Leu Leu Pro Lys Ser Leu Ile Trp Arg Leu Ile Ile Val Gly
            180                 185                 190

Ser Tyr Ile Ala Met Gly Ile Ile His Phe Leu Asp Tyr Tyr Val Ser
        195                 200                 205

Pro Pro Ser Lys Tyr Pro Asp Leu Trp Val Leu Ala Asn Cys Ser Leu
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Gly Phe Ser Cys Phe Val Thr Phe Trp Ile Trp Asn Asn Tyr
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<210> 93
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<213> Arabidopsis thaliana

<400> 93

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Ala Asn Phe Trp Cys Thr Thr Ser Ile Leu Ile Lys Trp Lys Asn Leu
            20                  25                  30

Phe Thr Thr Gln Ser Leu Lys Ser Ile Ser Leu Ala Ala Thr Ile Leu
        35                  40                  45

Ala Ser Leu Pro Ser Met Val Gln Gln Ile Leu Ser Pro Ser Asn Glu
    50                  55                  60

Gly Phe Leu Tyr Gly Leu Leu Asn Ser Ser Met Ala Phe Tyr Leu Phe
65                  70                  75                  80

Ser Phe Gln Val His Glu Lys Ser Ile Leu Met Pro Phe Leu Ser Ala
                85                  90                  95

Thr Leu Leu Ala Leu Lys Leu Pro Asp His Phe Ser His Leu Thr Tyr
            100                 105                 110

Tyr Ala Leu Phe Ser Met Phe Pro Leu Leu Cys Arg Asp Lys Leu Leu
        115                 120                 125

Ile Pro Tyr Leu Thr Leu Ser Phe Leu Phe Thr Val Ile Tyr His Ser
    130                 135                 140

Pro Gly Asn His His Ala Ile Gln Lys Thr Asp Val Ser Phe Phe Ser
145                 150                 155                 160

Phe Lys Asn Phe Pro Gly Tyr Val Phe Leu Leu Arg Thr His Phe Phe
                165                 170                 175

Ile Ser Val Val Leu His Val Leu Tyr Leu Thr Ile Lys Pro Pro Gln
            180                 185                 190
```

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Lys Tyr Pro Phe Leu Phe Glu Ala Leu Ile Met Ile Leu Cys Phe Ser
        195                 200                 205

Tyr Phe Ile Met Phe Ala Phe Tyr Thr Asn Tyr
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<213> Kluyveromyces lactis

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Phe Gly Gly Tyr Lys Asn Leu Val Gln Ser Met His Arg Ile Phe Pro
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Phe Ala Arg Gly Ile Phe Glu Asp Lys Val Ala Asn Phe Trp Cys Val
         35                  40                  45

Ser Asn Ile Phe Ile Lys Tyr Arg Asn Leu Phe Thr Gln Lys Asp Leu
     50                  55                  60

Gln Leu Tyr Ser Leu Leu Ala Thr Val Ile Gly Leu Leu Pro Ser Phe
 65                  70                  75                  80

Ile Ile Thr Phe Leu Tyr Pro Lys Arg His Leu Leu Pro Tyr Ala Leu
                 85                  90                  95

Ala Ala Cys Ser Met Ser Phe Phe Leu Phe Ser Phe Gln Val His Glu
            100                 105                 110

Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Thr Ser
        115                 120                 125

Arg Asp Trp Asn Val Leu Ser Leu Val Cys Trp Ile Asn Asn Val Ala
    130                 135                 140

Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys Asp Asn Leu Val Leu Gln
145                 150                 155                 160

Tyr Gly Val Met Phe Met Val Thr Pro Arg Phe Leu Pro Lys Phe Leu
                165                 170                 175

Thr Pro Gly Pro Ser Ile Ser Asp Ile Asp Val Asp Tyr Arg Arg Ala
            180                 185                 190

Ser Leu Leu Pro Lys Ser Leu Ile Trp Arg Leu Ile Ile Val Gly Ser
        195                 200                 205
```

```
Tyr Ile Ala Met Gly Ile Ile His Phe Leu Asp Tyr Tyr Val Ser Pro
    210                 215                 220

Pro Ser Lys Tyr Pro Asp Leu Trp Val Leu Ala Asn Cys Ser Leu Gly
225                 230                 235                 240

Phe Ser Cys Phe Val Thr Phe Trp Ile Trp Asn Asn
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<210> 95
<211> 259
<212> PRT
<213> Homo sapiens

<400> 95

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Val Lys Leu Ala Cys Ile Val Val Ala Ser Phe Val Leu Cys Trp Leu
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Pro Phe Phe Thr Glu Arg Glu Gln Thr Leu Gln Val Leu Arg Arg Leu
            20                  25                  30

Phe Pro Val Asp Arg Gly Leu Phe Glu Asp Lys Val Ala Asn Ile Trp
        35                  40                  45

Cys Ser Phe Asn Val Phe Leu Lys Ile Lys Asp Ile Leu Pro Arg His
    50                  55                  60

Ile Gln Leu Ile Met Ser Phe Cys Phe Thr Phe Leu Ser Leu Leu Pro
65                  70                  75                  80

Ala Cys Ile Lys Leu Ile Leu Gln Pro Ser Ser Lys Gly Phe Lys Phe
                85                  90                  95

Thr Leu Val Ser Cys Ala Leu Ser Phe Phe Leu Phe Ser Phe Gln Val
            100                 105                 110

His Glu Lys Ser Ile Leu Leu Val Ser Leu Pro Val Cys Leu Val Leu
        115                 120                 125

Ser Glu Ile Pro Phe Met Ser Thr Trp Phe Leu Leu Val Ser Thr Phe
    130                 135                 140

Ser Met Leu Pro Leu Leu Leu Lys Asp Glu Leu Leu Met Pro Ser Val
145                 150                 155                 160

Val Thr Thr Met Ala Phe Phe Ile Ala Cys Val Thr Ser Phe Ser Ile
                165                 170                 175

Phe Glu Lys Thr Ser Glu Glu Glu Leu Gln Leu Lys Ser Phe Ser Ile
            180                 185                 190

Ser Val Arg Lys Tyr Leu Pro Cys Phe Thr Phe Leu Ser Arg Ile Ile
        195                 200                 205

Gln Tyr Leu Phe Leu Ile Ser Val Ile Thr Met Val Leu Leu Thr Leu
    210                 215                 220
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Met Thr Val Thr Leu Asp Pro Pro Gln Lys Leu Pro Asp Leu Phe Ser
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Val Leu Val Cys Phe Val Ser Cys Leu Asn Phe Leu Phe Phe Leu Val
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Tyr Phe Asn

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<211> 1617
<212> DNA
<213> Mus musculus

<400> 96
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<210> 97
<211> 536
<212> PRT
<213> Mus musculus

<400> 97
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Pro Arg Glu Leu Ala Ser Leu Ser Pro Asn Leu Ile Ser Ser Phe Phe
          35                  40                  45

Trp Asn Asn Ala Pro Val Thr Pro Gln Ala Ser Pro Glu Pro Gly Asp
      50                  55                  60

Pro Asp Leu Leu Arg Thr Pro Leu Tyr Ser His Ser Pro Leu Leu Gln
 65                  70                  75                  80

Pro Leu Ser Pro Ser Lys Ala Thr Glu Glu Leu His Arg Val Asp Phe
                 85                  90                  95

Val Leu Pro Glu Asp Thr Thr Glu Tyr Phe Val Arg Thr Lys Ala Gly
            100                 105                 110

Gly Val Cys Phe Lys Pro Gly Thr Arg Met Leu Glu Lys Pro Ser Pro
        115                 120                 125

Gly Arg Thr Glu Glu Lys Thr Glu Val Ser Glu Gly Ser Ser Ala Arg
    130                 135                 140

Gly Pro Ala Arg Arg Pro Met Arg His Val Leu Ser Ser Arg Glu Arg
145                 150                 155                 160

Leu Gly Ser Arg Gly Thr Arg Arg Lys Trp Val Glu Cys Val Cys Leu
                165                 170                 175

Pro Gly Trp His Gly Pro Ser Cys Gly Val Pro Thr Val Val Gln Tyr
            180                 185                 190

Ser Asn Leu Pro Thr Lys Glu Arg Leu Val Pro Arg Glu Val Pro Arg
        195                 200                 205

Arg Val Ile Asn Ala Ile Asn Ile Asn His Glu Phe Asp Leu Leu Asp
    210                 215                 220

Val Arg Phe His Glu Leu Gly Asp Val Val Asp Ala Phe Val Val Cys
225                 230                 235                 240

Asp Ser Asn Phe Thr Ala Tyr Gly Glu Pro Arg Pro Leu Lys Phe Arg
                245                 250                 255

Glu Met Leu Thr Asn Gly Thr Phe Glu Tyr Ile Arg His Lys Val Leu
            260                 265                 270

Tyr Val Phe Leu Asp His Phe Pro Pro Gly Gly Arg Gln Asp Gly Trp
        275                 280                 285

Ile Ala Asp Asp Tyr Leu Arg Thr Phe Leu Thr Gln Asp Gly Val Ser
    290                 295                 300

Arg Leu Arg Asn Leu Arg Pro Asp Asp Val Phe Ile Ile Asp Asp Ala
305                 310                 315                 320

Asp Glu Ile Pro Ala Arg Asp Gly Val Leu Phe Leu Lys Leu Tyr Asp
                325                 330                 335
```

```
Gly Trp Thr Glu Pro Phe Ala Phe His Met Arg Lys Ser Leu Tyr Gly
            340                 345                 350

Phe Phe Trp Lys Gln Pro Gly Thr Leu Glu Val Val Ser Gly Cys Thr
        355                 360                 365

Met Asp Met Leu Gln Ala Val Tyr Gly Leu Asp Gly Ile Arg Leu Arg
    370                 375                 380

Arg Arg Gln Tyr Tyr Thr Met Pro Asn Phe Arg Gln Tyr Glu Asn Arg
385                 390                 395                 400

Thr Gly His Ile Leu Val Gln Trp Ser Leu Gly Ser Pro Leu His Phe
                405                 410                 415

Ala Gly Trp His Cys Ser Trp Cys Phe Thr Pro Glu Gly Ile Tyr Phe
            420                 425                 430

Lys Leu Val Ser Ala Gln Asn Gly Asp Phe Pro Arg Trp Gly Asp Tyr
        435                 440                 445

Glu Asp Lys Arg Asp Leu Asn Tyr Ile Arg Ser Leu Ile Arg Thr Gly
    450                 455                 460

Gly Trp Phe Asp Gly Thr Gln Gln Glu Tyr Pro Pro Ala Asp Pro Ser
465                 470                 475                 480

Glu His Met Tyr Ala Pro Lys Tyr Leu Leu Lys Asn Tyr Asp Gln Phe
                485                 490                 495

Arg Tyr Leu Leu Glu Asn Pro Tyr Arg Glu Pro Lys Ser Thr Val Glu
            500                 505                 510

Gly Gly Arg Gln Asn Gln Gly Ser Asp Gly Arg Ser Ser Ala Val Arg
        515                 520                 525

Gly Lys Leu Asp Thr Ala Glu Gly
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<210> 98
<211> 2115
<212> DNA
<213> Homo sapiens

<400> 98

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<210> 99
<211> 535
<212> PRT
<213> Homo sapiens

<400> 99

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Ser Phe Leu Thr Leu Ser Trp Tyr Thr Thr Trp Gln Asn Gly Lys Glu
             20                  25                  30

Lys Leu Ile Ala Tyr Gln Arg Glu Phe Leu Ala Leu Lys Glu Arg Leu
         35                  40                  45

Arg Ile Ala Glu His Arg Ile Ser Gln Arg Ser Ser Glu Leu Asn Thr
     50                  55                  60

Ile Val Gln Gln Phe Lys Arg Val Gly Ala Glu Thr Asn Gly Ser Lys
 65                  70                  75                  80

Asp Ala Leu Asn Lys Phe Ser Asp Asn Thr Leu Lys Leu Leu Lys Glu
                 85                  90                  95

Leu Thr Ser Lys Lys Ser Leu Gln Val Pro Ser Ile Tyr Tyr His Leu
            100                 105                 110

Pro His Leu Leu Lys Asn Glu Gly Ser Leu Gln Pro Ala Val Gln Ile
        115                 120                 125

Gly Asn Gly Arg Thr Gly Val Ser Ile Val Met Gly Ile Pro Thr Val
    130                 135                 140
```

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Lys Arg Glu Val Lys Ser Tyr Leu Ile Glu Thr Leu His Ser Leu Ile
145                 150                 155                 160

Asp Asn Leu Tyr Pro Glu Glu Lys Leu Asp Cys Val Ile Val Val Phe
                165                 170                 175

Ile Gly Glu Thr Asp Ile Asp Tyr Val His Gly Val Val Ala Asn Leu
            180                 185                 190

Glu Lys Glu Phe Ser Lys Glu Ile Ser Ser Gly Leu Val Glu Val Ile
        195                 200                 205

Ser Pro Pro Glu Ser Tyr Tyr Pro Asp Leu Thr Asn Leu Lys Glu Thr
    210                 215                 220

Phe Gly Asp Ser Lys Glu Arg Val Arg Trp Arg Thr Lys Gln Asn Leu
225                 230                 235                 240

Asp Tyr Cys Phe Leu Met Met Tyr Ala Gln Glu Lys Gly Ile Tyr Tyr
                245                 250                 255

Ile Gln Leu Glu Asp Asp Ile Ile Val Lys Gln Asn Tyr Phe Asn Thr
            260                 265                 270

Ile Lys Asn Phe Ala Leu Gln Leu Ser Ser Glu Glu Trp Met Ile Leu
        275                 280                 285

Glu Phe Ser Gln Leu Gly Phe Ile Gly Lys Met Phe Gln Ala Pro Asp
    290                 295                 300

Leu Thr Leu Ile Val Glu Phe Ile Phe Met Phe Tyr Lys Glu Lys Pro
305                 310                 315                 320

Ile Asp Trp Leu Leu Asp His Ile Leu Trp Val Lys Val Cys Asn Pro
                325                 330                 335

Glu Lys Asp Ala Lys His Cys Asp Arg Gln Lys Ala Asn Leu Arg Ile
            340                 345                 350

Arg Phe Arg Pro Ser Leu Phe Gln His Val Gly Leu His Ser Ser Leu
        355                 360                 365

Ser Gly Lys Ile Gln Lys Leu Thr Asp Lys Asp Tyr Met Lys Pro Leu
    370                 375                 380

Leu Leu Lys Ile His Val Asn Pro Pro Ala Glu Val Ser Thr Ser Leu
385                 390                 395                 400

Lys Val Tyr Gln Gly His Thr Leu Glu Lys Thr Tyr Met Gly Glu Asp
                405                 410                 415

Phe Phe Trp Ala Ile Thr Pro Ile Ala Gly Asp Tyr Ile Leu Phe Lys
            420                 425                 430

Phe Asp Lys Pro Val Asn Val Glu Ser Tyr Leu Phe His Ser Gly Asn
        435                 440                 445
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Gln Glu His Pro Gly Asp Ile Leu Leu Asn Thr Thr Val Glu Val Leu
    450                 455                 460

Pro Phe Lys Ser Glu Gly Leu Glu Ile Ser Lys Glu Thr Lys Asp Lys
465                 470                 475                 480

Arg Leu Glu Asp Gly Tyr Phe Arg Ile Gly Lys Phe Glu Asn Gly Val
                485                 490                 495

Ala Glu Gly Met Val Asp Pro Ser Leu Asn Pro Ile Ser Ala Phe Arg
            500                 505                 510

Leu Ser Val Ile Gln Asn Ser Ala Val Trp Ala Ile Leu Asn Glu Ile
        515                 520                 525

His Ile Lys Lys Ala Thr Asn
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<210> 100
<211> 3226
<212> DNA
<213> Mus musculus

<400> 100

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acaaaacagg aagagggaat tgagccaatt gggaaggact ttggggccga tcctaaacca 2640
attaatttat ttatttggga ggatgggggc gggctcggga gggaggagag gggttgaaca 2700
gtttcctttt gttcctcact gttaattcgc ccaccttcgg gcccttcttg ttctgcagcg 2760
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tagaatgctt gcatagcata aatgaagtcc tgggttccat ccccagcacc acataaatgc 2940
aggtaagaaa cagagtcagg aggaccaagc attctccttg gctacataac aaaagcaagg 3000
cctttgtccc catgtcttgg ctacaagaga ccctatctca gaaaattgtg gggggggagg 3060
gggggaaat ggccttgaaa acacagccag tcactgtcac tgcattgcca gaactggtgg 3120
atcccaggtg tgcttggcag ataacagcta aaaggcacat aaccttggtg gggaaataaa 3180
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```

<210> 101
<211> 740
<212> PRT
<213> Mus musculus

<400> 101

```
Met Ala Phe Phe Ser Pro Trp Lys Leu Ser Ser Gln Lys Leu Gly Phe
  1               5                  10                  15

Phe Leu Val Thr Phe Gly Phe Ile Trp Gly Met Met Leu Leu His Phe
             20                  25                  30

Thr Ile Gln Gln Arg Thr Gln Pro Glu Ser Ser Ser Met Leu Arg Glu
         35                  40                  45

Gln Ile Leu Asp Leu Ser Lys Arg Tyr Ile Lys Ala Leu Ala Glu Glu
     50                  55                  60

Asn Arg Asp Val Val Asp Gly Pro Tyr Ala Gly Val Met Thr Ala Tyr
 65                  70                  75                  80

Asp Leu Lys Lys Thr Leu Ala Val Leu Leu Asp Asn Ile Leu Gln Arg
                 85                  90                  95

Ile Gly Lys Leu Glu Ser Lys Val Asp Asn Leu Val Asn Gly Thr Gly
            100                 105                 110

Ala Asn Ser Thr Asn Ser Thr Thr Ala Val Pro Ser Leu Val Ser Leu
        115                 120                 125

Glu Lys Ile Asn Val Ala Asp Ile Ile Asn Gly Val Gln Glu Lys Cys
    130                 135                 140

Val Leu Pro Pro Met Asp Gly Tyr Pro His Cys Glu Gly Lys Ile Lys
145                 150                 155                 160
```

```
Trp Met Lys Asp Met Trp Arg Ser Asp Pro Cys Tyr Ala Asp Tyr Gly
                165                 170                 175

Val Asp Gly Thr Ser Cys Ser Phe Phe Ile Tyr Leu Ser Glu Val Glu
            180                 185                 190

Asn Trp Cys Pro Arg Leu Pro Trp Arg Ala Lys Asn Pro Tyr Glu Glu
        195                 200                 205

Ala Asp His Asn Ser Leu Ala Glu Ile Arg Thr Asp Phe Asn Ile Leu
    210                 215                 220

Tyr Gly Met Met Lys Lys His Glu Glu Phe Arg Trp Met Arg Leu Arg
225                 230                 235                 240

Ile Arg Arg Met Ala Asp Ala Trp Ile Gln Ala Ile Lys Ser Leu Ala
                245                 250                 255

Glu Lys Gln Asn Leu Glu Lys Arg Lys Arg Lys Lys Ile Leu Val His
            260                 265                 270

Leu Gly Leu Leu Thr Lys Glu Ser Gly Phe Lys Ile Ala Glu Thr Ala
        275                 280                 285

Phe Ser Gly Gly Pro Leu Gly Glu Leu Val Gln Trp Ser Asp Leu Ile
    290                 295                 300

Thr Ser Leu Tyr Leu Leu Gly His Asp Ile Arg Ile Ser Ala Ser Leu
305                 310                 315                 320

Ala Glu Leu Lys Glu Ile Met Lys Lys Val Val Gly Asn Arg Ser Gly
                325                 330                 335

Cys Pro Thr Val Gly Asp Arg Ile Val Glu Leu Ile Tyr Ile Asp Ile
            340                 345                 350

Val Gly Leu Ala Gln Phe Lys Lys Thr Leu Gly Pro Ser Trp Val His
        355                 360                 365

Tyr Gln Cys Met Leu Arg Val Leu Asp Ser Phe Gly Thr Glu Pro Glu
    370                 375                 380

Phe Asn His Ala Ser Tyr Ala Gln Ser Lys Gly His Lys Thr Pro Trp
385                 390                 395                 400

Gly Lys Trp Asn Leu Asn Pro Gln Gln Phe Tyr Thr Met Phe Pro His
                405                 410                 415

Thr Pro Asp Asn Ser Phe Leu Gly Phe Val Val Glu Gln His Leu Asn
            420                 425                 430

Ser Ser Asp Ile His His Ile Asn Glu Ile Lys Arg Gln Asn Gln Ser
        435                 440                 445

Leu Val Tyr Gly Lys Val Asp Ser Phe Trp Lys Asn Lys Lys Ile Tyr
    450                 455                 460
```

```
Leu Asp Ile Ile His Thr Tyr Met Glu Val His Ala Thr Val Tyr Gly
465                 470                 475                 480

Ser Ser Thr Lys Asn Ile Pro Ser Tyr Val Lys Asn His Gly Ile Leu
                485                 490                 495

Ser Gly Arg Asp Leu Gln Phe Leu Leu Arg Glu Thr Lys Leu Phe Val
            500                 505                 510

Gly Leu Gly Phe Pro Tyr Glu Gly Pro Ala Pro Leu Glu Ala Ile Ala
        515                 520                 525

Asn Gly Cys Ala Phe Leu Asn Pro Lys Phe Asn Pro Pro Lys Ser Ser
    530                 535                 540

Lys Asn Thr Asp Phe Phe Ile Gly Lys Pro Thr Leu Arg Glu Leu Thr
545                 550                 555                 560

Ser Gln His Pro Tyr Ala Glu Val Phe Ile Gly Arg Pro His Val Trp
                565                 570                 575

Thr Val Asp Leu Asn Asn Arg Glu Glu Val Glu Asp Ala Val Lys Ala
            580                 585                 590

Ile Leu Asn Gln Lys Ile Glu Pro Tyr Met Pro Tyr Glu Phe Thr Cys
        595                 600                 605

Glu Gly Met Leu Gln Arg Ile Asn Ala Phe Ile Glu Lys Gln Asp Phe
    610                 615                 620

Cys His Gly Gln Val Met Trp Pro Pro Leu Ser Ala Leu Gln Val Lys
625                 630                 635                 640

Leu Ala Glu Pro Gly Gln Ser Cys Lys Gln Val Cys Gln Glu Ser Gln
                645                 650                 655

Leu Ile Cys Glu Pro Ser Phe Phe Gln His Leu Asn Lys Glu Lys Asp
            660                 665                 670

Leu Leu Lys Tyr Lys Val Thr Cys Gln Ser Ser Glu Leu Tyr Lys Asp
        675                 680                 685

Ile Leu Val Pro Ser Phe Tyr Pro Lys Ser Lys His Cys Val Phe Gln
    690                 695                 700

Gly Asp Leu Leu Leu Phe Ser Cys Ala Gly Ala His Pro Thr His Gln
705                 710                 715                 720

Arg Ile Cys Pro Cys Arg Asp Phe Ile Lys Gly Gln Val Ala Leu Cys
                725                 730                 735

Lys Asp Cys Leu
            740
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<210> 102
<211> 4

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative retention signal peptide

<400> 102
Lys Asp Glu Leu
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<210> 103
<211> 60
<212> PRT
<213> Saccharomyces cerevisiae

<400> 103
Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser
1 5 10 15

Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro
20 25 30

Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp
35 40 45

Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro
50 55 60

<210> 104
<211> 58
<212> PRT
<213> Drosophila virilis

<400> 104
Leu Pro Phe Phe Leu Cys Asn Phe Ile Gly Val Ala Cys Ala Arg Ser
1 5 10 15

Leu His Tyr Gln Phe Tyr Ile Trp Tyr Phe His Ser Leu Pro Tyr Leu
20 25 30

Val Trp Ser Thr Pro Tyr Ser Leu Gly Val Arg Tyr Leu Ile Leu Gly
35 40 45

Ile Ile Glu Tyr Cys Trp Asn Thr Tyr Pro
50 55

<210> 105
<211> 60
<212> PRT
<213> Saccharomyces cerevisiae

<400> 105
Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser
1 5 10 15

```
Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro
             20                  25                  30

Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp
         35                  40                  45

Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro
     50                  55                  60
```

<210> 106
<211> 59
<212> PRT
<213> Drosophila melanogaster

<400> 106

```
Leu Pro Phe Phe Leu Cys Asn Leu Val Gly Val Ala Cys Ala Ser Arg
  1               5                  10                  15

Ser Leu His Tyr Gln Phe Tyr Val Trp Tyr Phe His Ser Leu Pro Tyr
             20                  25                  30

Leu Ala Trp Ser Thr Pro Tyr Ser Leu Gly Val Arg Cys Leu Ile Leu
         35                  40                  45

Gly Leu Ile Glu Tyr Cys Trp Asn Thr Tyr Pro
     50                  55
```